

## SEARCH REQUEST FORM

Requestor's Name: \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Date: \_\_\_\_\_ Phone: \_\_\_\_\_ Art Unit: \_\_\_\_\_

### Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

### STAFF USE ONLY

Date completed: 08-27-03  
Searcher: Beverly C 4994  
Terminal time: 20  
Elapsed time: \_\_\_\_\_  
CPU time: \_\_\_\_\_  
Total time: 23  
Number of Searches: \_\_\_\_\_  
Number of Databases: 1

#### Search Site

\_\_\_\_ STIC  
\_\_\_\_ CM-1  
\_\_\_\_ Pre-S

#### Type of Search

\_\_\_\_ N.A. Sequence  
\_\_\_\_ A.A. Sequence  
\_\_\_\_ Structure  
\_\_\_\_ Bibliographic

#### Vendors

\_\_\_\_ IG  
\_\_\_\_ STN  
\_\_\_\_ Dialog  
\_\_\_\_ APS  
\_\_\_\_ Geninfo  
\_\_\_\_ SDC  
\_\_\_\_ DARC/Questel  
\_\_\_\_ Other CGN

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# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 102216

To: Minh-Tam Davis  
Location: CM1-8E12  
Art Unit: 1642  
Wednesday, August 27, 2003

Cas Serial Number: 09/700700

From: Beverly Shears  
Location: Biotech-Chem Library  
CM1-1E05  
Phone: 308-4994

beverly.shears@uspto.gov

### Search Notes

priority date:  
05/21/98

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 26, 2003, 12:08:16 ; Search time 9197 Seconds  
(without alignments)  
8611.617 Million cell updates/sec

Title: US-09-700-700-1  
Perfect score: 1936  
Sequence: 1 aatggtatgccaaacttaagt.....ggggcgccgcgactagtga 1936

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues  
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl :

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1836.4	94.9	2984	6	AR237420	AR237420 Sequence
2	1836.4	94.9	2984	6	AR260913	AR260913 Sequence
3	1836.4	94.9	2984	6	AR278444	AR278444 Sequence
4	1836.4	94.9	2984	6	AX106211	AX106211 Sequence
5	1836.4	94.9	2984	6	AX106554	AX106554 Sequence
6	1836.4	94.9	2984	6	AX140845	AX140845 Sequence
7	1836.4	94.9	2984	6	AX200705	AX200705 Sequence
8	1836.4	94.9	2984	6	AX267361	AX267361 Sequence
9	1834.2	94.7	80586	9	AC012574	AC012574 Homo sapi
10	1834.2	94.7	174445	9	AC051642	AC051642 Homo sapi
11	1832.6	94.7	184361	2	AC022597	AC022597 Homo sapi
12	1645.6	85.0	3266	9	AF247704	AF247704 Homo sapi
13	1388.8	71.7	2051	6	AR244306	AR244306 Sequence
14	641.2	33.1	1024	6	AR244053	AR244053 Sequence
15	628.4	32.5	1024	6	AR244068	AR244068 Sequence
16	628.2	32.4	1024	6	AR244054	AR244054 Sequence
17	622	32.1	1024	6	AR244067	AR244067 Sequence
18	615.6	31.8	1013	6	AR243986	AR243986 Sequence
19	611.8	31.6	724	6	AX203340	AX203340 Sequence
20	584.6	30.2	948	6	AR243995	AR243995 Sequence
21	582.2	30.1	720	6	AR244291	AR244291 Sequence
22	581	30.0	744	6	AR244290	AR244290 Sequence
23	580.6	30.0	716	6	AX203323	AX203323 Sequence
24	544.4	28.1	663	6	AX203318	AX203318 Sequence
25	539.6	27.9	980	6	AR243991	AR243991 Sequence
26	488	25.2	691	6	AX203331	AX203331 Sequence
27	477	24.6	697	6	AX203332	AX203332 Sequence
28	476.8	24.6	579	6	AX203314	AX203314 Sequence
29	469.4	24.2	484	6	AR261002	AR261002 Sequence
30	469.4	24.2	484	6	AR278533	AR278533 Sequence
31	469.4	24.2	484	6	AX106653	AX106653 Sequence
32	469.4	24.2	484	6	AX140944	AX140944 Sequence
33	469.4	24.2	484	6	AX200804	AX200804 Sequence
34	469.4	24.2	484	6	AX267460	AX267460 Sequence
35	461.6	23.8	582	6	AX203333	AX203333 Sequence
36	447.4	23.1	553	6	AX203313	AX203313 Sequence
37	446.6	23.1	683	6	AX203345	AX203345 Sequence
38	426.2	22.0	731	6	AX203310	AX203310 Sequence
39	421.6	21.8	1020	6	AR244074	AR244074 Sequence
40	421.6	21.8	1021	6	AR244075	AR244075 Sequence
41	411	21.2	822	6	AR244195	AR244195 Sequence
42	378.2	19.5	497	6	AR244194	AR244194 Sequence
43	358.8	18.5	374	6	AX337002	AX337002 Sequence
44	358.8	18.5	374	11	G37241	G37241 SHGC-57295
45	357.6	18.5	375	6	BD121246	BD121246 EST and e

ALIGNMENTS

RESULT 1	AR237420	2984 bp	DNA	linear	PAT 20-DEC-2002
LOCUS	Sequence 335 from patent US 6465611.				
DEFINITION	AR237420				
ACCESSION	AR237420				
VERSION	AR237420.1	GI:27282078			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 2984)				
AUTHORS	Xu,J., Dillon,D.C. and Mitcham,J.L.				
TITLE	Compounds for immunotherapy of prostate cancer and methods for their use				
JOURNAL	Patent: US 6465611-A 335 15-OCT-2002;				

FEATURES		Location/Qualifiers	
source	1..2984	/organism="unknown"	
BASE COUNT	837 a	659 c	645 g
ORIGIN	842 t 1 others		
Query Match 94.9%; Score 1836.4; DB 6; Length 2984;			
Best Local Similarity 99.0%; Pred. No. 0;			
Matches 1897; Conservative 0; Mismatches 12; Indels 7; Gaps 5;			
Qy	1	AATGTATGCCAACTTAAGTATTATACAGGGTGGCCCAATAGAACAGATGCACTCGCTG	60
Db	1067	AATGTATGCCAACTTAAGTATTATACAGGGTGGCCCAATAGAACAGATGCACTCGCTG	1126
Qy	61	TGATTTTAAGACAAGCTGTATAAACAAGAACTCCACTGCAAGAGGGGCGCGGCCAGGA	120
Db	1127	TGATTTTAAGACAAGCTGTATAAACAAGAACTCCACTGCAAGAGGGGCGCGGCCAGGA	1186
Qy	121	GAATCTCCGCTTGTCCAAGACAGGGCCCTAAGGAGGCTCTCCACACTGTCTGTAGGGCT	180
Db	1187	GAATCTCCGCTTGTCCAAGACAGGGCCCTAAGGAGGCTCTCCACACTGTCTGTAGGGCT	1246
Qy	181	GTTCGATTTTTTATTAGTAGAAGTGAAGAGCCCTCTTCTCAACTTTTTTCCCTTGGGC	240
Db	1247	GTTCGATTTTTTATTAGTAGAAGTGAAGAGCCCTCTTCTCAACTTTTTTCCCTTGGGC	1306
Qy	241	TGGAGAAATTAGAATCAGAAAGTTTCTCGAGTTTTCAGGCTATCATATATACGTATCCT	300
Db	1307	TGGAGAAATTAGAATCAGAAAGTTTCTCGAGTTTTCAGGCTATCATATATACGTATCCT	1366
Qy	301	GAAGGCAACATAATCTTCTCCCTCCCTTTTAAATTTTGTGTTCTTTTTCGAGCAA	360
Db	1367	GAAGGCAACATAATCTTCTCCCTCCCTTTTAAATTTTGTGTTCTTTTTCGAGCAA	1426
Qy	361	TTACTCACTAAGGGCTTCATTTTAGTCCAGATTTTGTAGTCTGGCTGCACCTAATTATG	420
Db	1427	TTACTCACTAAGGGCTTCATTTTAGTCCAGATTTTGTAGTCTGGCTGCACCTAATTATG	1486
Qy	421	CCTCGCTTATTAGCCGAGATCTGGTCTTTTNTGTTTNTTNTTNTTNTTNTTNTTNTTNTT	480
Db	1487	CCTCGCTTATTAGCCGAGATCTGGTCTTTTNTGTTTNTTNTTNTTNTTNTTNTTNTTNTT	1544
Qy	481	CAAGCTTTATCTGTCTTGAATTTTAAAGAGTTTGGGGCGAGATTCGAATTTGGGCTA	540
Db	1545	CAAGCTTTATCTGTCTTGAATTTTAAAGAGTTTGGGGCGAGATTCGAATTTGGGCTA	1603
Qy	541	AAAGACATGCAATTTTAAACTAGGCAACTCTTATTTCTTCTTTTAAATAATACATAGC	600
Db	1604	AAAGACATGCAATTTTAAACTAG--CAACTCTTATTTCTTCTTTTAAATAATACATAGC	1661
Qy	601	ATTAAATCCCAATCCTATTAAAGACCTGACAGCTTGAGAGGTCACTACTGCAATTTAT	660
Db	1662	ATTAAATCCCAATCCTATTAAAGACCTGACAGCTTGAGAGGTCACTACTGCAATTTAT	1721
Qy	661	AGGACCTTCTGGTGGTCTGCTGTATAGTTTGAAGTCTGACAACTCTTGAATTTCTTTGC	720
Db	1722	AGGACCTTCTGGTGGTCTGCTGTATAGTTTGAAGTCTGACAACTCTTGAATTTCTTGC	1781
Qy	721	ATGCAAGAGGATAAGAGTATTGAAATTTTCAAGAGGAAGAAACACAGCGCAGAAATGAAG	780
Db	1782	ATGCAAGAGGATAAGAGTATTGAAATTTTCAAGAGGAAGAAACACAGCGCAGAAATGAAG	1841
Qy	781	GGCCAGGCTTACTGAGGCTGTCCAGTGGAGGCTCATGGGTGGACATGGAAGAAGGCG	840
Db	1842	GGCCAGGCTTACTGA--GCTGTCCAAGTGGAGGCTCATGGGTGGACATGGAAGAAGGCG	1900
Qy	841	AGCTTAGGCCCTGGGGAGCCAGTCCACTGAGCAAGCAAGGACTGAGTGAGCCTTTTTC	900
Db	1901	AGCTTAGGCCCTGGGGAGCCAGTCCACTGAGCAAGCAAGGACTGAGTGAGCCTTTTTC	1960
Qy	901	AGGAAAGGCTAAGAAAAAGGAAAAACCAATTTTAAACACAAACAGAACTGTCCAAATGC	960
Db	1961	AGGAAAGGCTAAGAAAAAGGAAAAACCAATTTTAAACACAAACAGAACTGTCCAAATGC	2020
Qy	961	TTTGGGAACCTGTGTTTATTGCTTATAATGGGTCCCAAAATGGGTAACTAGACTTCAGA	1020
Db	2021	TTTGGGAACCTGTGTTTATTGCTTATAATGGGTCCCAAAATGGGTAACTAGACTTCAGA	2080
Qy	1021	GAGAAATGACGACAGAGCAAGAGAAATCTGGCTGTCTCTTCCATTTTCACTCTGTATCT	1080
Db	2081	GAGAAATGACGACAGAGCAAGAGAAATCTGGCTGTCTCTTCCATTTTCACTCTGTATCT	2140
Qy	1081	CAGGTGAGCTGTAGAGGGGAGACATTTAGAAAAAATGAAACAAACAAATTAATAAT	1140
Db	2141	CAGGTGAGCTGTAGAGGGGAGACATTTAGAAAAAATGAAACAAACAAATTAATAAT	2200
Qy	1141	GAGGTACGCTCAGGCGCTGGGAGTCTCTTGACTCCACTTAATTCGTTTGTAGTGAATA	1200
Db	2201	GAGGTACGCTCAGGCGCTGGGAGTCTCTTGACTCCACTTAATTCGTTTGTAGTGAATA	2260
Qy	1201	CCCTTCAATTTTCTTTTATTAGAGGGCCAGCTTACTGTGTGGCAAAATTTGCCAAT	1260
Db	2261	CCCTTCAATTTTCTTTTATTAGAGGGCCAGCTTACTGTGTGGCAAAATTTGCCAAT	2320
Qy	1261	AAGTTAAATGAAAGTTGGCCAAATTTTCAACCCCAATTTTCTGTGTGGGTCCCAATTGCA	1320
Db	2321	AAGTTAAATGAAAGTTGGCCAAATTTTCAACCCCAATTTTCTGTGTGGGTCCCAATTGCA	2380
Qy	1321	ATGTTCAATGTCACAGTGTGCTGACACCGAGAGTACTAGCCAGCAAAAGGCGAGGG	1380
Db	2381	ATGTTCAATGTCACAGTGTGCTGACACCGAGAGTACTAGCCAGCAAAAGGCGAGGG	2440
Qy	1381	TAGCCTGAATTTGCTTTCTGCTCTTTTACATTTCTTTTAAATTAAGCATTTTGTGCTCAGTC	1440
Db	2441	TAGCCTGAATTTGCTTTCTGCTCTTTTACATTTCTTTTAAATTAAGCATTTTGTGCTCAGTC	2500
Qy	1441	CCTACTGAGTACTCTTTCTCTCCCTCTCTGCAATTTTCTTTTCACTTGCATTTGCGTCTCC	1500
Db	2501	CCTACTGAGTACTCTTTCTCTCCCTCTCTGCAATTTTCTTTTCACTTGCATTTGCGTCTCC	2560
Qy	1501	AAGGATTACACATTTTCACTGTGATGATATTTGTTTGCAGNAGAAAGAAAGTGTCTT	1560
Db	2561	AAGGATTACACATTTTCACTGTGATGATATTTGTTTGCAGNAGAAAGAAAGTGTCTT	2619
Qy	1561	TGTTTAAATTAATCTGTTTGTGAATCCATCTGCTTTTCCCATTTGGAACCTAGTCAATT	1620
Db	2620	TGTTTAAATTAATCTGTTTGTGAATCCATCTGCTTTTCCCATTTGGAACCTAGTCAATT	2679
Qy	1621	AACCCATCTGAACTGGTAGAAAAACATCTGAAGAGTCTATCAGCATCTGCAGAGG	1680
Db	2680	AACCCATCTGAACTGGTAGAAAAACATCTGAAGAGTCTATCAGCATCTGCAGAGG	2739
Qy	1681	TGAATTTGATGGTCTCAGAACCATTTTCAACCCAGCAGCCTGTTTCTATCTCTGTTTAAATA	1740
Db	2740	TGAATTTGATGGTCTCAGAACCATTTTCAACCCAGCAGCCTGTTTCTATCTCTGTTTAAATA	2799
Qy	1741	AAATTAGTTGGGTCTCTACATGCAATAACAAACCCCTGCTCCAATCTGTCAATAAAGTC	1800
Db	2800	AAATTAGTTGGGTCTCTACATGCAATAACAAACCCCTGCTCCAATCTGTCAATAAAGTC	2859
Qy	1801	TGTGACTTGAAGTTTAGTCAGCACCCCAACAACTTTATTTTCTATGTTGTTTTTGA	1860
Db	2860	TGTGACTTGAAGTTTAGTCAGCACCCCAACAACTTTATTTTCTATGTTGTTTTTGA	2919
Qy	1861	ACATATGAGTGTGTTTGAATAAAGTACCCATGCTTTTATTAAAAAANAANAANA	1916
Db	2920	ACATATGAGTGTGTTTGAATAAAGTACCCATGCTTTTATTAAAAAANAANAANA	2975
RESULT 2			
AR260913			
LOCUS			
DEFINITION			
AR260913			
ACCESSION			
VERSION			
KEYWORDS			
Sequence 335 from patent US 6321716.			
2984 bp DNA linear PAT 29-JAN-2003			

SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 2984)  
AUTHORS Mashiki, Z. and Harada, J.  
TITLE Negative pressure control apparatus for engine mounted in vehicle  
JOURNAL Patent: US 6321716-A 335 27-NOV-2001;  
FEATURES Location/Qualifiers  
source 1. 2984  
BASE COUNT 837 a 659 c 645 g 842 t 1 others  
ORIGIN

Query Match 94.9%; Score 1836.4; DB 6; Length 2984;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 1897; Conservative 0; Mismatches 12; Indels 7; Gaps 5;

QY 1 AATGGTATGCCAACTTAAGTATTTACAGGGTGGCCCAATAGACAGATGCACTCGCTG 60  
DB 1067 AATGGTATGCCAACTTAAGTATTTACAGGGTGGCCCAATAGACAGATGCACTCGCTG 1126

QY 61 TGATTTTAAGACAAGCTGTATAACAGAACTCCCACTGCAAGAGGNGGGCCGGGCCAGGA 120  
DB 1127 TGATTTTAAGACAAGCTGTATAACAGAACTCCCACTGCAAGAGGNGGGCCGGGCCAGGA 1186

QY 121 GAATCTCCGCTTGTCCAAGACAGGGGCTTAAGAGGGTCTCCACACTGCTGCTAGGGGCT 180  
DB 1187 GAATCTCCGCTTGTCCAAGACAGGGGCTTAAGAGGGTCTCCACACTGCTGCTAGGGGCT 1246

QY 181 GTTGCATTTTTTATTAGTAGAAGTGAAGAGGCTCTTCTCAACTTTTTTCCCTTGGGC 240  
DB 1247 GTTGCATTTTTTATTAGTAGAAGTGAAGAGGCTCTTCTCAACTTTTTTCCCTTGGGC 1306

QY 241 TGGAGAAATTAGAAATCAGAAATTTCTGGAGTTTTCAGGCTATCATATATACGTATCT 300  
DB 1307 TGGAGAAATTAGAAATCAGAAATTTCTGGAGTTTTCAGGCTATCATATATACGTATCT 1366

QY 301 GAAAGGCAACATAATTTCTTCCCTCCCTTTTAAATTTTGTGTTCTTTTGGCAGCA 360  
DB 1367 GAAAGGCAACATAATTTCTTCCCTCCCTTTTAAATTTTGTGTTCTTTTGGCAGCA 1426

QY 361 TTAATCACTAAGGGCTTCAATTTAGTCCAGATTTTATGCTGGCTGCACCTAATATG 420  
DB 1427 TTAATCACTAAGGGCTTCAATTTAGTCCAGATTTTATGCTGGCTGCACCTAATATG 1486

QY 421 CCTCGCTTATTAGCCGAGATCTGCTCTTTTNTGTTTNTTTTNTTNTTCCGCTCCC 480  
DB 1487 CCTCGCTTATTAGCCGAGATCTGCTCTTTTNTGTTTNTTTTNTTNTTCCGCTCCC 1544

QY 481 CAAAGCTTTATCTGTCTGACTTTTAAAGTTTGGGGCAGATTTCTGAATTTGGGCTA 540  
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QY 541 AAAGACATGCAATTTTAAACTAGGCAACTTCTTATTTCTTCTTTTAAATATACATAG 600  
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QY 601 ATTAATATCCCAATCTTATTAAAGACCTGACAGCTTGAAGGTCACACTGCAATTTAT 660  
DB 1662 ATTAATATCCCAATCTTATTAAAGACCTGACAGCTTGAAGGTCACACTGCAATTTAT 1721

QY 661 AGGACCTTCTGGTGTCTGCTGTATAGTTTGAAGTCTGACATCTTGGAGATCTTTG 720  
DB 1722 AGGACCTTCTGGTGTCTGCTGTATAGTTTGAAGTCTGACATCTTGGAGATCTTTG 1781

QY 721 ATCAGAGAGGTAAGAGTATTTGATTTTACAGAGGAGAACACAGCGGCAATGAAG 780  
DB 1782 ATCAGAGAGGTAAGAGTATTTGATTTTACAGAGGAGAACACAGCGGCAATGAAG 1841

QY 781 GGCCAGGCTTACTAGGCTGTCAGTGGGGCTCATGGGTGGGACATGGAAAGAGGC 840  
DB 1842 GGCCAGGCTTACTGA-GCTGTCCAGTGGGGGCTCATGGGTGGGACATGGAAAGAGGC 1900

QY 841 AGCTTAGGCCCTGGGAGCCCACTGAGCAAGAGGAGCTAGTGAGCCTTTTGC 900  
DB 1901 AGCTTAGGCCCTGGGAGCCCACTGAGCAAGAGGAGCTAGTGAGCCTTTTGC 1960

QY 901 AGGAAAGGCTAAGAAAGGAAACCACTTCTAAACACAAAGAAACCTGTCCAAATGC 960  
DB 1961 AGGAAAGGCTAAGAAAGGAAACCACTTCTAAACACAAAGAAACCTGTCCAAATGC 2020

QY 961 TTTGGGAACTGTGTTTATTGGCCTATAATGGGTCCCAAAATGGTAACCTAGACTTCAG 1020  
DB 2021 TTTGGGAACTGTGTTTATTGGCCTATAATGGGTCCCAAAATGGTAACCTAGACTTCAG 2080

QY 1021 GAGATGACGAGAGAGAAAGAGAAATCTGGCTGTCTTCCATTTTCTGTTATCT 1080  
DB 2081 GAGATGACGAGAGAGAAAGAGAAATCTGGCTGTCTTCCATTTTCTGTTATCT 2140

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QY 1141 GAGGTACGCTGAGGCTGGGAGTCTCTTGACTCCACTACTTAATTCCTGTTAGTGAGAAA 1200  
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QY 1201 CCTTCAATTTTCTTTTATTAGAGGGCCAGCTTACTGTGTGGCAAAATTTGCCAACAT 1260  
DB 2261 CCTTCAATTTTCTTTTATTAGAGGGCCAGCTTACTGTGTGGCAAAATTTGCCAACAT 2320

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DB 2321 AAGTTAATAGAAAGTTGGCCAAATTTTCAAGGGCTTCTGTGTGGTGGGCTCCACATTGCA 2380

QY 1321 ATGTTCAATGCGACGCTGCTGACACCGAGAGTACTAGCCAGCAACAAAGGCGAGG 1380  
DB 2381 ATGTTCAATGCGACGCTGCTGACACCGAGAGTACTAGCCAGCAACAAAGGCGAGG 2440

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QY 1501 AAGGATTAACAAATTTCACTGTGATGTATTTGTGTCAGNAGAAAGAAAAAGTGTCTT 1560  
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QY 1561 TGTTTAAATTAATTTGGTTTGTGAATCCATCTTGTCTTTTCCCAATGGAACTAGTCATT 1620  
DB 2620 TGTTTAAATTAATTTGGTTTGTGAATCCATCTTGTCTTTTCCCAATGGAACTAGTCATT 2679

QY 1621 AACCCATCTGAACTGTGAGAAAAACATCTGAAAGCTAGTCTATCAGCATCTGCAGG 1680  
DB 2680 AACCCATCTGAACTGTGAGAAAAACATCTGAAAGCTAGTCTATCAGCATCTGCAGG 2739

QY 1681 TGAATTTGATGTTTCTCAGAACCAATTTCAACCCAGACAGCTGTTTCTATCTGTTTAAATA 1740  
DB 2740 TGAATTTGATGTTTCTCAGAACCAATTTCAACCCAGACAGCTGTTTCTATCTGTTTAAATA 2799

QY 1741 AATTAGTTGGGTTCTCTACATGCAATAACAAACCTGCTCCAATCTGTGCACATAAAGTTC 1800  
DB 2800 AATTAGTTGGGTTCTCTACATGCAATAACAAACCTGCTCCAATCTGTGCACATAAAGTTC 2859

QY 1801 TGTGACTTGAAGTTAGTACAGCAACCCCAACAACTTATTTTTTCTATGTGTTTTTGTGA 1860  
DB 2860 TGTGACTTGAAGTTAGTACAGCAACCCCAACAACTTATTTTTTCTATGTGTTTTTGTGA 2919

QY 1861 ACATATGATGTTTTTGAATAAAGTACCCATGCTCTTTTAAATAAATAAATAAATAA 1916  
DB 2920 ACATATGATGTTTTTGAATAAAGTACCCATGCTCTTTTAAATAAATAAATAAATAA 2975

RESULT 3  
AR278444  
LOCUS  
DEFINITION  
Sequence 335 from patent US 6512094.  
AR278444  
ACCESSION  
AR278444.1 GI:29712690  
VERSION  
KEYWORDS  
Unknown.  
SOURCE  
ORGANISM  
Unclassified.  
REFERENCE  
1 (bases 1 to 2984)  
AUTHORS  
Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,  
Kaios, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,  
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W.,  
Hepler, W.T. and Henderson, R.A.  
TITLE  
Compositions and methods for the therapy and diagnosis of prostate  
cancer  
JOURNAL  
Patent: US 6512094-A 335 28-JAN-2003;  
FEATURES  
Location/Qualifiers  
1..2984  
/organism="unknown"  
BASE COUNT 837 a 659 c 645 g 842 t 1 others  
ORIGIN

Query Match 94.9%; Score 1836.4; DB 6; Length 2984;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 1897; Conservative 0; Mismatches 12; Indels 7; Gaps 5;

QY 1 AATGATGCAACTTAAGTATTTACAGGGTGGCCCAATAGACAGATGCACTCGCTG 60  
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ACCESSION AX106211  
VERSION AX106211.1 GI:13921900  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Skeiky, Y.A., Xu, J., Cheever, M.A. and Reed, S.G.  
TITLE Compositions and methods for wti specific immunotherapy  
JOURNAL Patent: WO 0125273-A 349 12-APR-2001;  
CORIXA CORPORATION (US)  
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Location/Qualifiers  
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BASE COUNT 837 a 659 c 645 g 842 t 1 others  
ORIGIN

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Matches 1897; Conservative 0; Mismatches 12; Indels 7; Gaps 5;

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LOCUS AX140845 2984 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 335 from Patent WO0134802.
ACCESSION AX140845
VERSION AX140845.1 GI:14280952
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H.,
Skelky,Y.A. and Wang,A.
TITL Composition and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0134802-A 335 17-MAY-2001;
CORIXA CORPORATION (US)
FEATURES
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Best Local Similarity 99.0%; Pred. No. 0;
Matches 1897; Conservative 0; Mismatches 12; Indels 7; Gaps 5;
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RESULT 7  
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LOCUS  
DEFINITION Sequence 335 from Patent WO0151633.  
ACCESSION AX200705  
VERSION AX200705.1 GI:15390594  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Xu, J., Dillon, D. C., Mitcham, J. L., Harlocker, S. L., Jiang, Y., Reed, S. G., Kalos, M. D., Fanger, G. R., Day, C. H., Retter, M. W., Skolk, J. A., Skeiky, Y. A., Wang, A. and Meagher, M. J.  
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer  
JOURNAL Patent: WO 0151633-A 335 19-JUL-2001;  
CORIXA CORPORATION (US)  
FEATURES  
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BASE COUNT 837 a 659 c 645 g 842 t 1 others

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Matches 1897; Conservative 0; Mismatches 12; Indels 7; Gaps 5;  
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DEFINITION Homo sapiens chromosome 8, clone RP11-213G6, linear PRI 01-APR-2002  
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AC012574.7 GI:19852145  
KEYWORDS HTG.

## SOURCE

ORGANISM Homo sapiens (human)

## REFERENCE

AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,

TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

JOURNAL 1 (bases 1 to 80586)

REFERENCE 1 (bases 1 to 80586)

AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.

TITLE Homo sapiens chromosome 8, clone RP11-213G6

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 80586)

AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,

TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

JOURNAL 1 (bases 1 to 80586)

REFERENCE 1 (bases 1 to 80586)

AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,

TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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JOURNAL 1 (bases 1 to 80586)

REFERENCE 1 (bases 1 to 80586)

AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,

Center project name: L2354  
Center clone name: 213\_G\_6  
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Only the first 80.6 kilobases of this clone is being submitted.  
The remainder overlaps either accession number AC051642 [WICGR  
project L8828] or accession number AC012119 [WICGR project L2190].

## FEATURES

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Best Local Similarity 98.9%; Pred. No. 0;

Matches 1887; Conservative 0; Mismatches 13; Indels 8; Gaps 4;

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Db 10702 AATGTTATGCCAACTTAAGTATTTACGGTGGCCCAATAGAAACAAGATGACCTCGCTG 10643  
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Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., Locke, K., McDonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mienga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivari, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, K., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Testfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

## Direct Submission

Submitted (15-Apr-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 174445)

## JOURNAL

## REFERENCE

## AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Collangelo, M., Collins, S., Collumore, A., Cook, A., Cooke, P., DeArelano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lakocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

## Direct Submission

Submitted (17-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Dec 21, 2001 this sequence version replaced gi:16905345.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L8828

Center clone name: 593\_M\_2

## FEATURES

## source

## Location/Qualifiers

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/mol\_type="genomic DNA"

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DEFINITION Homo sapiens chromosome 8 clone RP11-19A13 map 8, WORKING DRAFT
ACCESSION AC022597
VERSION   AC022597.7 GI:22123001
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SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
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REFERENCE 1 (bases 1 to 184361)
          Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
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          Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J.,
          Zimmer, A. and Zody, M.
          Direct Submission
          Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome
          Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (bases 1 to 184361)
          Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
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TITLE  
JOURNAL

## COMMENT

Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Aug 6, 2002 this sequence version replaced gi:14010820.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information

Center project name: L4195

Center clone name: 19\_A\_13

----- Summary Statistics

Sequencing vector: M13; M77815; 3% of reads  
 Sequencing method: Plasmid; n/a; 97% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 180318 bases at least Q40  
 Consensus quality: 182555 bases at least Q30  
 Consensus quality: 183338 bases at least Q20  
 Insert size: 173000; agarose-fp  
 Insert size: 183761; sum-of-contigs  
 Quality coverage: 8.2 in Q20 bases; agarose-fp  
 Quality coverage: 7.8 in Q20 bas.

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 7 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 1054: contig of 1054 bp in length  
 1055 1154: gap of 100 bp  
 1155 2825: contig of 1671 bp in length  
 2826 2925: gap of 100 bp  
 2926 29148: contig of 26223 bp in length  
 29149 29248: gap of 100 bp  
 29249 59090: contig of 29842 bp in length  
 59091 59190: gap of 100 bp  
 59191 110096: contig of 50906 bp in length  
 110097 110196: gap of 100 bp  
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 149305 149404: gap of 100 bp  
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**KEYWORDS**  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 3266)  
**AUTHORS** Korkmaz,K.S., Korkmaz,C.G., Regnhildstveit,E., Kizildag,S.,  
 Pretlow,T.G. and Saatcioglu,F.  
**TITLE** Full-length cDNA sequence and genomic organization of human  
 NKX3.1-Alternative mRNA forms and regulation by both androgens and  
 estrogens  
**JOURNAL** Unpublished  
**REFERENCE** 2 (bases 1 to 3266)  
**AUTHORS** Korkmaz,K.S., Korkmaz,C.G. and Saatcioglu,F.  
**TITLE** Direct Submision  
**JOURNAL** Submitted (22-MAR-2000) University of Oslo, Biotechnology Center of  
 Oslo, Gaustadalleen 21, Oslo 0349, Norway  
**FEATURES**  
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DEFINITION Sequence 81 from patent US 6476207.  
ACCESSION AR244053  
VERSION AR244053.1 GI:27291840  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1024)  
AUTHORS Zhang, J., Astle, J.H., Carroll, E. III, Endege, W.O., Ford, D.M.,  
Monahan, J.E., Schlegel, R. and Steinmann, K.E.  
TITLE Genes and gene expression products that are differentially  
regulated in prostate cancer  
JOURNAL Patent: US 6476207-A 81 05-NOV-2002;  
FEATURES Location/Qualifiers  
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BASE COUNT 248 a 239 c 210 g 281 t 46 others  
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DEFINITION Sequence 96 from patent US 6476207.  
ACCESSION AR244068  
VERSION AR244068.1 GI:27291855  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1024)  
AUTHORS Zhang, J., Astle, J.H., Carroll, E. III, Endege, W.O., Ford, D.M.,  
Monahan, J.E., Schlegel, R. and Steinmann, K.E.  
TITLE Genes and gene expression products that are differentially  
regulated in prostate cancer  
JOURNAL Patent: US 6476207-A 96 05-NOV-2002;  
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Job time : 9204 secs

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PT  
Diagnosis

XX

Diagnosing, monitoring, and staging prostate cancer -  
XX

Claim 6; Page 22-23; 30pp; English.

PS The present sequence represents a human prostate specific gene (PSG)  
 XX (gene ID 244673). The mRNA levels for PSG are about 20 fold higher  
 CC in the prostate than in other tissues. The PSG mRNA was found to be  
 CC overexpressed in prostate tumour samples. The specification describes  
 CC a method for diagnosing the presence of, or metastatic potential of,  
 CC prostate cancer in a patient. The method comprises measuring PSG levels  
 CC in a cell, tissue or bodily fluid sample of the patient and a control  
 CC (i.e. a normal human without cancer), where increased PSG levels in  
 CC the patient compared to the control is associated with the presence of,  
 CC or metastasis of prostate cancer. The method can also be used for  
 CC staging prostate cancer in a patient. The methods are used to detect,  
 CC monitor, stage and give a prognosis for prostate cancer.

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Query Match 99.7%; Score 1930; DB 21; Length 1936;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1936; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 GAATCTCCGCTTGTCCAGACAGGGCTTAAGAGGGTCTCCACACTGTGCTAGGGGCT 180

DB 121 GAATCTCCGCTTGTCCAGACAGGGCTTAAGAGGGTCTCCACACTGTGCTAGGGGCT 180

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QY 481 CAAAGCTTTATCTGTCTGATCTTTTAAATAAGTTTGGGGCAGATTCGAAATGGGCTA 540

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QY 601 ATTAAATCCCAATCTTATTAAAGACCTGACAGCTTGAGAGGTCACCTACGCAATTTAT 660

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DB 1261 AAGTTAATAGAAAGTTGGCCAAATTTACCCCAATTTCTGTGGTTTGGGCTCCACATTGCA 1320

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DB 1381 TAGCCTGAATTTGCTTCTGCTCTTTTCAATTTCTTTTAAATAAGCAATTTAGTGTCTAGTC 1440

QY 1441 CCTACTGAGTACTCTTTCTCTCCCTCTCTGAAATTTAAATTTCTTTCACTGCAATTTTC 1500

DB 1441 CCTACTGAGTACTCTTTCTCTCCCTCTCTGAAATTTAAATTTCTTTCACTGCAATTTTC 1500

QY 1501 AAGGATTACACATTTCACTGTGATGTATATTGTGTGAGGAAAGAAAAAGTGTCTT 1560

DB 1501 AAGGATTACACATTTCACTGTGATGTATATTGTGTGAGGAAAGAAAAAGTGTCTT 1560

QY 1561 TGTTTAAATTTACTTGTGTTGTAATCCATCTGCTTTTCCCATTTGGAACTAGTCATT 1620

DB 1561 TGTTTAAATTTACTTGTGTTGTAATCCATCTGCTTTTCCCATTTGGAACTAGTCATT 1620

QY 1621 AACCCATCTCTGAACTGCTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGG 1680

DB 1621 AACCCATCTCTGAACTGCTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGG 1680

QY 1681 TGAATTTGATGTTTCTCAGAACCAATTTCAACCAGACAGCCTGTTCTATCTCTGTTAATA 1740

DB 1681 TGAATTTGATGTTTCTCAGAACCAATTTCAACCAGACAGCCTGTTCTATCTCTGTTAATA 1740

QY 1741 AATTAGTTTGGGTTCTCTACATGCAATAACAAACCTGCTCCAATCTCTGCAATAAAGTC 1800

DB 1741 AATTAGTTTGGGTTCTCTACATGCAATAACAAACCTGCTCCAATCTCTGCAATAAAGTC 1800

QY 1801 TGTGACTTGAAGTTTAGTACAGCAACCCCAACCAACTTTATTTTTCTATGTTGTTTTTTCGA 1860

DB 1801 TGTGACTTGAAGTTTAGTACAGCAACCCCAACCAACTTTATTTTTCTATGTTGTTTTTTCGA 1860

QY 1861 ACATATGAGTGTGTTGAAAAATAAAGTACCCTGCTTTTATAAAAAANAAGGGGC 1920

```
Db 1861 ACATATGAGTGTGTAATAAAGTACCCATGCTTTATTAATAAATAAAGGGC 1920
QY 1921 GGCCGCGACTAGTGA 1936
Db 1921 GGCCGCGACTAGTGA 1936

RESULT 2
AAA06564
ID AAA06564 standard; cDNA; 2984 BP.
XX
AC AAA06564;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:335.
XX
KW Human, prostate cancer; diagnosis; tumour; gene therapy; detection;
KW immunogenic; cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200004149-A2.
XX
PD 27-JAN-2000.
XX
PF 14-JUL-1999; 99WO-US15838.
XX
PR 14-JUL-1998; 98US-0115453.
PR 14-JUL-1998; 98US-0116134.
PR 23-SEP-1998; 98US-0159812.
PR 23-SEP-1998; 98US-0159822.
PR 15-JAN-1999; 98US-0232149.
PR 15-JAN-1999; 98US-0232880.
PR 09-APR-1999; 99US-0288946.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Harlocker SL, Yuqiu J, Xu J, Mitcham JL;
XX
DR WPI; 2000-171268/15.
XX
PT New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein -
XX
PS Claim 50; Page 207-208; 263pp; English.
XX
CC The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumour protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AAA06241 to AAA06691 and
CC AA082000 to AA082020 represent sequences used in the exemplification of
CC the present invention.
XX
SQ Sequence 2984 BP; 837 A; 659 C; 645 G; 842 T; 1 other;

Query Match 94.9%; Score 1836.4; DB 21; Length 2984;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1897; Conservative 0; Mismatches 12; Indels 7; Gaps 5;

QY 1 AATGGTATGCCAACTTAAGTATTACAGGTGGCCCAATAGAACAAAGATGCATCGCTG 60
Db 1067 AATGGTATGCCAACTTAAGTATTACAGGTGGCCCAATAGAACAAAGATGCATCGCTG 1126
QY 61 TGATTTTAAGCAAGCTGTATATAACAGAACTCCACTGCAAGGGGCGGCCGAGGA 120
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Db 1127 TGAATTTAAGCAAGCTGTATATAACAGAACTCCACTGCAAGAGGGGGCCCGGCCAGGA 1186
QY 121 GAATCTCCGCTTGTCCAAGACAGGGGCCCTAAGAGAGGCTCCACACTGCTGCTAGGGGCT 180
Db 1187 GAATCTCCGCTTGTCCAAGACAGGGGCCCTAAGAGAGGCTCCACACTGCTGCTAGGGGCT 1246
QY 181 GTTGCAATTTTTATTAGTAGAAGTGGAAAGCCCTCTTCTCAACTTTTTTCCCTTTGGGC 240
Db 1247 GTTGCAATTTTTATTAGTAGAAGTGGAAAGCCCTCTTCTCAACTTTTTTCCCTTTGGGC 1306
QY 241 TCGAGAAATTTAGAAATCAGAAAGTTTCTGAGATTTTCAGGCTATCATATATACGTATCT 300
Db 1307 TCGAGAAATTTAGAAATCAGAAAGTTTCTGAGATTTTCAGGCTATCATATATACGTATCT 1366
QY 301 GAAAGCAACATAATTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
Db 1367 GAAAGCAACATAATTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1426
QY 361 TTACTCACTAAAGGGCTTCATTTTATAGTCCAGATTTTATAGTCTGGCTGCACCTAATATG 420
Db 1427 TTACTCACTAAAGGGCTTCATTTTATAGTCCAGATTTTATAGTCTGGCTGCACCTAATATG 1486
QY 421 CCTCGCTTATTTAGCCCGAGATCTGGTCTTTTGTGTTTGTGTTTGTGTTTGTGTTTGTG 480
Db 1487 CCTCGCTTATTTAGCCCGAGATCTGGTCTTTTGTGTTTGTGTTTGTGTTTGTGTTTGTG 1544
QY 481 CAAAGCTTTATCTGCTTGAATTTTAAAGAGTTTGGGGCGAGATTCGAAATTTGGGCTA 540
Db 1545 CAAAGCTTTATCTGCTTGAATTTTAAAGAGTTTGGGGCGAGATTCGAAATTTGGGCTA 1603
QY 541 AAAGACATGCATTTTAAAGCTAGGCACTCTTATTTCTTTCTTTAAATAATACATAGC 600
Db 1604 AAAGACATGCATTTTAAAGCTAGGCACTCTTATTTCTTTCTTTAAATAATACATAGC 1661
QY 601 ATTAATCCAAATCCTATTTAAAGACCTGACAGCTTGAGAAAGTGCATCTGCAATTTAT 660
Db 1662 ATTAATCCAAATCCTATTTAAAGACCTGACAGCTTGAGAAAGTGCATCTGCAATTTAT 1721
QY 661 AGGACCTTCTGCTGTTCTGCTGTTTCAAGTCTGACAAATCCTTCAGAAATCTTTGTC 720
Db 1722 AGGACCTTCTGCTGTTCTGCTGTTTCAAGTCTGACAAATCCTTCAGAAATCTTTGTC 1781
QY 721 ATGACAGAGGTAAGAGGTATTGGATTTTCAAGAGGAAGAACACAGCGCAGAAATGAAG 780
Db 1782 ATGACAGAGGTAAGAGGTATTGGATTTTCAAGAGGAAGAACACAGCGCAGAAATGAAG 1841
QY 781 GGCCAGGCTTACTGAGGCTGTCCAGTGGAGGCTCATGGGTGGGACATGGAAAAGAGGC 840
Db 1842 GGCCAGGCTTACTGA-GCTGTCCAGTGGAGGCTCATGGGTGGGACATGGAAAAGAGGC 1900
QY 841 AGCCTAGGCCCTGGGAGCCCACTGACGCAAGGAGGCTGAGTGAGGCTTTTTCG 900
Db 1901 AGCCTAGGCCCTGGGAGCCCACTGACGCAAGGAGGCTGAGTGAGGCTTTTTCG 1960
QY 901 AGCAAAAGCTTAAGAAAAGGAAAACCAATTTTAAACACAACAAGAACTGTCCTCAATGC 960
Db 1961 AGCAAAAGCTTAAGAAAAGGAAAACCAATTTTAAACACAACAAGAACTGTCCTCAATGC 2020
QY 961 TTTGGAACTGTTTATTGCTTATAATGGGTCCCAAAATGGGTAACTAGACTTCAG 1020
Db 2021 TTTGGAACTGTTTATTGCTTATAATGGGTCCCAAAATGGGTAACTAGACTTCAG 2080
QY 1021 GAGAAATGACAGAGCAAGGAGAAATCTGGCTGCTCTTCCATTTTCTTCTTCTTCTTCT 1080
Db 2081 GAGAAATGACAGAGCAAGGAGAAATCTGGCTGCTCTTCCATTTTCTTCTTCTTCTTCT 2140
QY 1081 CAGGTGAGCTGTTAGAGGGGAGACATTAGAAAAAATGAAAAAACAACAACAATTAAT 1140
Db 2141 CAGGTGAGCTGTTAGAGGGGAGACATTAGAAAAAATGAAAAAACAACAACAATTAAT 2200
QY 1141 GAGGTACGCTGAGGCTCGGAGTCTCTTGACTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1200
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Db 1487 CCTCGCTATTATAGCCGAGATCTGGTCTTTTTT - TTTTTTTTTTTTTTTCGCTCC 1544  
Qy 481 CAAAGCTTTATCTGTCTTGACTTTTTTAAAGTTTGGGGCAGATCTCGAATTTGGGCTA 540  
Db 1545 CAAAGCTTTATCTGTCTTGACTTTTTTAAAGTTTGGGGCAGATCTCGAATTT - GGCTA 1603  
Qy 541 AAAGACATGCAATTTTAAAGCTAGGCAACTTCTTATTTCTTCTTAAAGATACATAGC 600  
Db 1604 AAAGACATGCAATTTTAAAGCTAGGCAACTTCTTATTTCTTCTTAAAGATACATAGC 1661  
Qy 601 ATTAAATCCCAATCTTATTAAAGACCTGACAGCTTGAAGGTCACTACTGCAATTTAT 660  
Db 1662 ATTAAATCCCAATCTTATTAAAGACCTGACAGCTTGAAGGTCACTACTGCAATTTAT 1721  
Qy 661 AGACCTTCTGGTGTCTGCTTACGTTTGAAGTCTGACAACTCTTGAGAACTTTTCG 720  
Db 1722 AGACCTTCTGGTGTCTGCTTACGTTTGAAGTCTGACAACTCTTGAGAACTTTTCG 1781  
Qy 721 ATGCAGAGGCTAAGAGGTATTGGATTTTACAGAGGAAGAACACAGCGCAGAAATGAAG 780  
Db 1782 ATGCAGAGGCTAAGAGGTATTGGATTTTACAGAGGAAGAACACAGCGCAGAAATGAAG 1841  
Qy 781 GGCACGCTTACTGAGGCTGTCCAGTGGAGGCTCATGGTGGGACATGGAAGAAAGAGGC 840  
Db 1842 GGCACGCTTACTGA - GCTGTCCAGTGGAGGCTCATGGTGGGACATGGAAGAAAGAGGC 1900  
Qy 841 AGCTAGGCCCTGGGAGGCCAGTCCACTGAGCAAGGAGTCTGAGTGGAGCTTTTTCG 900  
Db 1901 AGCTAGGCCCTGGGAGGCCAGTCCACTGAGCAAGGAGTCTGAGTGGAGCTTTTTCG 1960  
Qy 901 AGGAAAGGCTAAGAAAGGAAAGAACCATTTCTAAACACAAAGAACTGTCCTAAATGC 960  
Db 1961 AGGAAAGGCTAAGAAAGGAAAGAACCATTTCTAAACACAAAGAACTGTCCTAAATGC 2020  
Qy 961 TTGGGAACTGTCTTATTGCTTATTAATGGTCCCAATGGTAACTGAGCTTTCACA 1020  
Db 2021 TTGGGAACTGTCTTATTGCTTATTAATGGTCCCAATGGTAACTGAGCTTTCACA 2080  
Qy 1021 GAGATGACAGAGCAAGGAGAAATCTGGTCTCTTCCATTTTCATTTCTGTTATCT 1080  
Db 2081 GAGATGACAGAGCAAGGAGAAATCTGGTCTCTTCCATTTTCATTTCTGTTATCT 2140  
Qy 1081 CAGGTGAGCTGGTAGGGGAGACATTAGAAATAATGAAACAAACAAATCTACTAAT 1140  
Db 2141 CAGGTGAGCTGGTAGGGGAGACATTAGAAATAATGAAACAAACAAATCTACTAAT 2200  
Qy 1141 GAGGTACGCTGAGGCTGGGAGTCTCTGACTCCACTACTTAATTCGTTTGTAGGAA 1200  
Db 2201 GAGGTACGCTGAGGCTGGGAGTCTCTGACTCCACTACTTAATTCGTTTGTAGGAA 2260  
Qy 1201 CCTTCAATTTCTTTTATTAGAGGCCAGCTTACTGTGTGGCAAAATTCGCAACAT 1260  
Db 2261 CCTTCAATTTCTTTTATTAGAGGCCAGCTTACTGTGTGGCAAAATTCGCAACAT 2320  
Qy 1261 AGTTTAATAGAAAGTTGGCAATTTCAACCCATTTCTGTGTGTGGCTCCACATGCA 1320  
Db 2321 AGTTTAATAGAAAGTTGGCAATTTCAACCCATTTCTGTGTGTGGCTCCACATGCA 2380  
Qy 1321 ATGTTCAATGCCAGTGTCTGACACCGGAGTACTAGCCAGCAAAAGGAGG 1380  
Db 2381 ATGTTCAATGCCAGTGTCTGACACCGGAGTACTAGCCAGCAAAAGGAGG 2440  
Qy 1381 TAGCCTGAATTTCTCTCTCTTTTACATTTCTTTTAAATTAAGCATTTAGTGTCTCAGTC 1440  
Db 2441 TAGCCTGAATTTCTCTCTCTTTTACATTTCTTTTAAATTAAGCATTTAGTGTCTCAGTC 2500  
Qy 1441 CTTACTGAGTACTTTTCTCTCCCTCTCTGAAATTAATTTCTTCAACTTGCATTTTCG 1500  
Db 2501 CTTACTGAGTACTTTTCTCTCCCTCTCTGAAATTAATTTCTTCAACTTGCATTTTCG 2560  
Qy 1501 AAGGATTACATTTTCACTGTGATGATTTGTTGAGGAAAGAAAGAAAGTGTCTT 1560  
Db 2561 AAGGATTACATTTTCACTGTGATGATTTGTTGAGGAAAGAAAGAAAGTGTCTT 2619

Qy 1561 TCTTTAAATTACTTGGTTTGTGAATCCATCTTGTCTTTTCCCATTTGGAACCTAGTCAAT 1620  
Db 2620 TCTTTAAATTACTTGGTTTGTGAATCCATCTTGTCTTTTCCCATTTGGAACCTAGTCAAT 2679  
Qy 1621 AACCCATCTCTCAACTGGTAGAAGAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAG 1680  
Db 2680 AACCCATCTCTCAACTGGTAGAAGAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAG 2739  
Qy 1681 TGAATTTGATGTTCTCTCAGAACCATTTACCCAGACAGCTCTTCTATCTCTGTTTAAATA 1740  
Db 2740 TGAATTTGATGTTCTCTCAGAACCATTTACCCAGACAGCTCTTCTATCTCTGTTTAAATA 2799  
Qy 1741 AATTAGTTTGGTTTCTCTACATGATCAATAACAAACCTGTCTCCATCTGTCAATAAAGTC 1800  
Db 2800 AATTAGTTTGGTTTCTCTACATGATCAATAACAAACCTGTCTCCATCTGTCAATAAAGTC 2859  
Qy 1801 TGTGACTTGAAGTTTGTAGTCAGCACCCCAACCAAACTTTATTTTCTATCTGTTTGTGCA 1860  
Db 2860 TGTGACTTGAAGTTTGTAGTCAGCACCCCAACCAAACTTTATTTTCTATCTGTTTGTGCA 2919  
Qy 1861 ACATATGAGTGTTTTGAATAAAGTACCATGTCTTTATTAAATAAATAAATAA 1916  
Db 2920 ACATATGAGTGTTTTGAATAAAGTACCATGTCTTTATTAGAAAAAATAAATAA 2975

## RESULT 4

AAH93680  
ID AAH93680 standard; cDNA; 2984 BP.  
XX  
AC AAH93680;  
XX  
DT 04-OCT-2001 (first entry)  
XX Human prostate-specific cDNA sequence P705P.  
DE Human; prostate cancer; prostate-specific; diagnosis; vaccine;  
KW cytosolic; gene therapy; metastasis; ss.  
XX Homo sapiens.  
OS  
XX WO200151633-A2.  
PN  
XX 19-JUL-2001.  
PD  
XX 16-JAN-2001; 2001WO-US01574.  
PF  
XX 14-JAN-2000; 2000US-0483672.  
PR  
XX (CORI-) CORIXA CORP.  
PA  
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;  
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;  
PI Wang A, Meagher MJ;  
XX  
DR WPI; 2001-425873/45.  
XX  
PT New polynucleotide encoding a prostate-specific protein, for  
PT diagnosing, monitoring and treating prostate cancer in a patient and  
PT for use in vaccines -  
XX  
PS Claim 1; Page 333-334; 543pp; English.

XX The present invention describes polynucleotide sequences (I) which encode  
CC prostate-specific proteins (II). (I) and (II) have cytosolic activity,  
CC and can be used in vaccine production and gene therapy. (I), (II),  
CC antibodies to (II), fusion proteins comprising (II), and isolated  
CC T cells prepared using (I) or (II) are used to treat cancer in a patient.  
CC (I) and the antibodies are also used in the detection of cancer in a  
CC patient. The cancer that is diagnosed or treated is particularly  
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or  
CC (I) can be used for monitoring the progression of cancer in a patient.  
CC (I) and (II) can also be used to improve diagnostic and therapeutic

CC methods for prostate cancer. They can indicate the level of metastasis  
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to  
CC AAH01318 represent polynucleotide and amino acid sequences used in the  
CC exemplification of the present invention.  
XX  
SQ Sequence 2984 BP; 837 A; 659 C; 645 G; 842 T; 1 other;

Query Match		94.9%;	Score 1836.4;	DB 22;	Length 2984;
Best Local Similarity		99.0%;	Pred. No. 0;		
Matches 1897;		Conservative	0;	Mismatches	12; Indels 7; Gaps 5;
QY	1	AATGGTATGCCAATTAAGTATTTACAGGGTGGCCCAATAAGAACAAAGATGCACTCGCTG	60		
DB	1067	AATGGTATGCCAATTAAGTATTTACAGGGTGGCCCAATAAGAACAAAGATGCACTCGCTG	1126		
QY	61	TGATTTTAAGACAAAGCTGTATAAACAAGACTCCACTGCAAGAGGNGGCGCGGCAGGA	120		
DB	1127	TGATTTTAAGACAAAGCTGTATAAACAAGACTCCACTGCAAGAGGNGGCGCGGCAGGA	1186		
QY	121	GAATCTCCGCTGTGTCACAGACAGGGGCTTAAGAGGGGTCTCCACACTGCTGCTAGGGGCT	180		
DB	1187	GAATCTCCGCTGTGTCACAGACAGGGGCTTAAGAGGGGTCTCCACACTGCTGCTAGGGGCT	1246		
QY	181	GTTCGATTTTTTATTTAGTAGAAGTGGAAAGGCTCTTCTCAACTTTTTCCTTGGGC	240		
DB	1247	GTTCGATTTTTTATTTAGTAGAAGTGGAAAGGCTCTTCTCAACTTTTTCCTTGGGC	1306		
QY	241	TGGAGAATTTAGAATCAGAAGTTTCCTCGAGTTTTCAGGCTATCATATACGTATTCCT	300		
DB	1307	TGGAGAATTTAGAATCAGAAGTTTCCTCGAGTTTTCAGGCTATCATATACGTATTCCT	1366		
QY	301	GAAGGCAACATAAATCTCTCCCTCTTTTAAATTTTGTCTTTTTCAGCAAA	360		
DB	1367	GAAGGCAACATAAATCTCTCTCCCTCTTTTAAATTTTGTCTTTTTCAGCAAA	1426		
QY	361	TTACTCACTAAGGGCTTCATTTAGTCCAGATTTTGTAGTCTGCTGACCTAATATG	420		
DB	1427	TTACTCACTAAGGGCTTCATTTAGTCCAGATTTTGTAGTCTGCTGACCTAATATG	1486		
QY	421	CCTGCTTTATTTAGCCGAGATCTGGTCTTTTNTCTTTTNTCTTTTTCCTGCTCCG	480		
DB	1487	CCTGCTTTATTTAGCCGAGATCTGGTCTTTTNTCTTTTNTCTTTTTCCTGCTCCG	1544		
QY	481	CAAGCTTTATCTGCTTTGACTTTTAAAGTTTGGGGGAGATCTGAATTTGGGCTA	540		
DB	1545	CAAGCTTTATCTGCTTTGACTTTTAAAGTTTGGGGGAGATCTGAATTTGGGCTA	1603		
QY	541	AAAGACATGCAATTTTAAACTAGGCACTTCTTATTTCTTTCTTTTAAATAACATAGC	600		
DB	1604	AAAGACATGCAATTTTAAACTAG--CAACTCTTATTTCTTTCTTTTAAATAACATAGC	1661		
QY	601	ATTAAATCCCAATCTTATTTAAGACCTGACAGCTTGAGAGGTCACTACTGCAATTTAT	660		
DB	1662	ATTAAATCCCAATCTTATTTAAGACCTGACAGCTTGAGAGGTCACTACTGCAATTTAT	1721		
QY	661	AGGACCTTCTGGTGGTCTGCTGTTAGTCTGCAATCTGCAATCTTGGAGATCTTTGC	720		
DB	1722	AGGACCTTCTGGTGGTCTGCTGTTAGTCTGCAATCTTGGAGATCTTCTTGGATCTTTGC	1781		
QY	721	ATCAGAGGAGGTAAGAGGTATTTGATTTTTCAGAGGAAGAACACAGCGAGAATGAAG	780		
DB	1782	ATCAGAGGAGGTAAGAGGTATTTGATTTTTCAGAGGAAGAACACAGCGAGAATGAAG	1841		
QY	781	GGCCAGGCTTACTGAGGCTGTCCAGTGGAGGCTCATGTTGGTGGGATGGAAGAGGCG	840		
DB	1842	GGCCAGGCTTACTGGA--GCTGTCCAGTGGAGGCTCATGTTGGTGGGATGGAAGAGGCG	1900		
QY	841	AGCCTAGGCGCTGGGAGGCCAGTCCACTGACAAAGGAGTGAAGTGGCTTTTTC	900		
DB	1901	AGCCTAGGCGCTGGGAGGCCAGTCCACTGACAAAGGAGTGAAGTGGCTTTTTC	1960		
QY	901	AGGAAAGGCTTAAGAAAAGGAAAACCACTTCTTAAACACACAGAACTCTCAAAATGC	960		

RESULT 5  
ID AAH84994  
XX AAH84994 standard; cdNA; 2984 BP.  
XX AAH84994;  
XX

DB	1961	AGGAAAAGCGCTAAGAAAAGGAAAAGCAATTTCTTAAACACACAAAGAAACCTGCTCAAATGC	2020
QY	961	TTTGGGAACCTGCTGTTTATTTGCCCTTATTAATGGGTCCCAAAATGGTAACTAGACTTCAGA	1020
DB	2021	TTTGGGAACCTGCTGTTTATTTGCCCTTATTAATGGGTCCCAAAATGGTAACTAGACTTCAGA	2080
QY	1021	GAGATGAGCAGAGAGCAAGAGGAATCTGGCTGCTCCATTTTCATTTCTGTTATCT	1080
DB	2081	GAGATGAGCAGAGAGCAAGAGGAATCTGGCTGCTCCATTTTCATTTCTGTTATCT	2140
QY	1081	CAGGTGAGCTGTGAGAGGAGGAGACATTAGAAAAAATGAAAAAACAATAAATTAATAAT	1140
DB	2141	CAGGTGAGCTGTGAGAGGAGGAGACATTAGAAAAAATGAAAAAACAATAAATTAATAAT	2200
QY	1141	GAGGTACGCTGAGGCTGCGAGTCTCTTGACTCCACTACTTAATTCGTTTGTAGTGAAGA	1200
DB	2201	GAGGTACGCTGAGGCTGCGAGTCTCTTGACTCCACTACTTAATTCGTTTGTAGTGAAGA	2260
QY	1201	CTTTTCAATTTTCTTTTATTTAGAGGGCAGCTTACTGTTGGTGGCAAAATTTGCCAACAT	1260
DB	2261	CTTTTCAATTTTCTTTTATTTAGAGGGCAGCTTACTGTTGGTGGCAAAATTTGCCAACAT	2320
QY	1261	AAGTAAATAGAAAGTTGGCCAAATTTTCAACCAATTTTCTGTTGGTGGCTCCCAATTGCA	1320
DB	2321	AAGTAAATAGAAAGTTGGCCAAATTTTCAACCAATTTTCTGTTGGTGGCTCCCAATTGCA	2380
QY	1321	ATGTTCAATGTCACGCTGCTGTGACACCGACGGAGTACTAGCCAGCACAAAGGCGAGG	1380
DB	2381	ATGTTCAATGTCACGCTGCTGTGACACCGACGGAGTACTAGCCAGCACAAAGGCGAGG	2440
QY	1381	TAGCCTGAAATTTGCTTCTGCTCTTACATTTCTTTTAAATAAGCAATTTAGTGTCTAGTC	1440
DB	2441	TAGCCTGAAATTTGCTTCTGCTCTTACATTTCTTTTAAATAAGCAATTTAGTGTCTAGTC	2500
QY	1441	CCTACTGAGTACTCTTTCTCTCCCTCTCTGTAATTTAACTTTCAACTTTGCAATTTGC	1500
DB	2501	CCTACTGAGTACTCTTTCTCTCCCTCTCTGTAATTTAACTTTCAACTTTGCAATTTGC	2560
QY	1501	AAGGATTTACACATTTCTGCTGATGATATTTGTTGTCAGNGAAAAAGAAAGTGTCTT	1560
DB	2561	AAGGATTTACACATTTCTGCTGATGATATTTGTTGTCAGNGAAAAAGAAAGTGTCTT	2619
QY	1561	TGTTTAAATTAATCTGTTGTTGTAATCCATCTTCTTTTCCCATTTGGAACTAGTCAAT	1620
DB	2620	TGTTTAAATTAATCTGTTGTTGTAATCCATCTTCTTTTCCCATTTGGAACTAGTCAAT	2679
QY	1621	AACCCATCTCTGAACTGGTGAAGAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGG	1680
DB	2680	AACCCATCTCTGAACTGGTGAAGAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGG	2739
QY	1681	TGAATTCGATGGTCTCAGAACCAATTTTCCAGCAGAGCTGTTCTATCTGTTTAAATA	1740
DB	2740	TGAATTCGATGGTCTCAGAACCAATTTTCCAGCAGAGCTGTTCTATCTGTTTAAATA	2799
QY	1741	AATTAGTTTGGGTCTCTACATGCAATAACAAACCCCTGCTCCAACTCTGTCACATAAAGTC	1800
DB	2800	AATTAGTTTGGGTCTCTACATGCAATAACAAACCCCTGCTCCAACTCTGTCACATAAAGTC	2859
QY	1801	TGTGACTTGAAGTTTGTAGTCAGACCCCAACCAAACTTTTCTATGTTGTTTTTGA	1860
DB	2860	TGTGACTTGAAGTTTGTAGTCAGACCCCAACCAAACTTTTCTATGTTGTTTTTGA	2919
QY	1861	ACATATGAGTGTGTTTGAATAAAGTACCCCATGCTTTTATTAATAAANAANAANA	1916
DB	2920	ACATATGAGTGTGTTTGAATAAAGTACCCCATGCTTTTATTAATAAANAANAANA	2975





Db 1901 AGCCTAGCCCTGGGAGCCAGTCCACTGAGCAAGCAAGGGACTGAGTGACCTTTTGC 1960  
Qy 901 AGGAAAGGCTAAGAAAAGGAAAAGCAATCTAAACACAAACAAAGAACTGTCAAATGC 960  
Db 1961 AGGAAAGGCTAAGAAAAGGAAAAGCAATCTAAACACAAACAAAGAACTGTCAAATGC 2020  
Qy 961 TTTGGGAACGTGTTTATTGCTTATATATGGTCCCCAAATGGTAACTAGACTTCAGA 1020  
Db 2021 TTTGGGAACGTGTTTATTGCTTATATATGGTCCCCAAATGGTAACTAGACTTCAGA 2080  
Qy 1021 GAGAATGACGAGAGCAAGAGGAGAACTCTGGCTGCTCCATTTTCATTCCTGTTATCT 1080  
Db 2081 GAGAATGACGAGAGCAAGAGGAGAACTCTGGCTGCTCCATTTTCATTCCTGTTATCT 2140  
Qy 1081 CAGGTGAGCTGGTAGAGGGGAGACATTTAGAAAAAATGAAACAAACAAACAAATTTACTAAT 1140  
Db 2141 CAGGTGAGCTGGTAGAGGGGAGACATTTAGAAAAAATGAAACAAACAAACAAATTTACTAAT 2200  
Qy 1141 GAGGTACGCTGAGGCTGGGAGTCTCTTGACTCCACTACTTAATTCGGTTTGTAGTGA 1200  
Db 2201 GAGGTACGCTGAGGCTGGGAGTCTCTTGACTCCACTACTTAATTCGGTTTGTAGTGA 2260  
Qy 1201 CCTTCAATTTCTTTTATTAGAGGGCCAGCTTACTGTGTGGGCAAAATTCGCAACAT 1260  
Db 2261 CCTTCAATTTCTTTTATTAGAGGGCCAGCTTACTGTGTGGGCAAAATTCGCAACAT 2320  
Qy 1261 AAGTTAATAGAAAGTTGGCCAAATTTCAACCCCATTTTCTGTGGTTTGGGCTCCACATTTGA 1320  
Db 2321 AAGTTAATAGAAAGTTGGCCAAATTTCAACCCCATTTTCTGTGGTTTGGGCTCCACATTTGA 2380  
Qy 1321 ATGTTCAATGCCACGTGCTGCTGACACCGAGTACTAGCCAGCAAAAGGCGAGG 1380  
Db 2381 ATGTTCAATGCCACGTGCTGCTGACACCGAGTACTAGCCAGCAAAAGGCGAGG 2440  
Qy 1381 TAGCCTGAATGCTTTCTGCTCTTTTCAATTTCTTTTAAATAAGCAATTTAGTGTCTCAGTC 1440  
Db 2441 TAGCCTGAATGCTTTCTGCTCTTTTCAATTTCTTTTAAATAAGCAATTTAGTGTCTCAGTC 2500  
Qy 1441 CCTACTGAGTACTTTCTCTCCCTCTCTGAAATTAATTTCTTCAACTTGAATTTGC 1500  
Db 2501 CCTACTGAGTACTTTCTCTCCCTCTCTGAAATTAATTTCTTCAACTTGAATTTGC 2560  
Qy 1501 AAGGATTACAAATTTCACTGTGATGATATATGTGTGCAAGGAAAAGAAAGTGTCTT 1560  
Db 2561 AAGGATTACAAATTTCACTGTGATGATATATGTGTGCA - AAAAAGGAAAGTGTCTT 2619  
Qy 1561 TGTTHAAATTTACTTGGTTGTGAATCCATCTGCTTTTCCCATTTGGAACCTAGTCAAT 1620  
Db 2620 TGTTHAAATTTACTTGGTTGTGAATCCATCTGCTTTTCCCATTTGGAACCTAGTCAAT 2679  
Qy 1621 AACCCATCTCTGAACCTGTAGAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGG 1680  
Db 2680 AACCCATCTCTGAACCTGTAGAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGG 2739  
Qy 1681 TGAATTTGATGTTCTCAGAACCAATTTCAACAGAGAGGCTGTTTCTATCTCTGTTTAA 1740  
Db 2740 TGAATTTGATGTTCTCAGAACCAATTTCAACAGAGAGGCTGTTTCTATCTCTGTTTAA 2799  
Qy 1741 AATTAGTTTGGGTTCTCTACATGATGATAACAAACCCCTGCTCCATCTGTGCATATAAAGTC 1800  
Db 2800 AATTAGTTTGGGTTCTCTACATGATGATAACAAACCCCTGCTCCATCTGTGCATATAAAGTC 2859  
Qy 1801 TGTGACTTCAAGTTTGTAGTCAGACACCCCAACCTTTTATTTTCTATGTTTGTGCA 1860  
Db 2860 TGTGACTTCAAGTTTGTAGTCAGACACCCCAACCTTTTATTTTCTATGTTTGTGCA 2919  
Qy 1861 ACATATGAGTGTGTTTGAATAAAGTACCCATGCTCTTTTATTAATAAATAAATAA 1916  
Db 2920 ACATATGAGTGTGTTTGAATAAAGTACCCATGCTCTTTTATTAATAAATAAATAA 2975

AAF86953  
ID AAF86953 standard; cDNA; 2984 BP.  
XX  
AC AAF86953;  
XX  
DT 06-JUL-2001 (first entry)  
XX  
DE Human P705P inventive antigen coding sequence SEQ ID NO: 349.  
XX  
KW Human; mouse; immunotherapy; cancer; leukaemia; WTI; Wilm's tumour gene;  
KW chromosome 11p13; zinc finger transcription factor; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200125273-A2.  
XX  
PD 12-APR-2001.  
XX  
PF 04-OCT-2000; 2000WO-US27465.  
XX  
PR 04-OCT-1999; 99US-0157459.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Skeiky YAW, Xu J, Cheever MA, Reed SG;  
XX  
DR WPI; 2001-328324/34.  
XX  
PT Polypeptide comprising part of the Wilm's Tumour gene product sequence is  
PT used in the diagnosis and treatment of malignant diseases e.g. leukemia  
PT and cancer associated with WTI  
XX  
PS Disclosure; Page 221-222; 228pp; English.  
XX  
CC The present invention describes compositions comprising peptides derived  
CC from the Wilm's tumour protein WTI and methods for their use in treating  
CC malignant diseases. Peptides derived from both the murine and human WTI  
CC proteins are provided. The human WTI gene is found on chromosome 11p13,  
CC and the protein was shown to be a zinc finger transcription factor. The  
CC immunogenic peptides of the invention are particularly useful in the  
CC diagnosis and treatment of cancer and leukaemia. The present sequence is  
CC a coding sequence used in the exemplification of the invention.  
XX  
SQ Sequence 2984 BP; 837 A; 659 C; 645 G; 842 T; 1 other;  
Query Match 94.9%; Score 1836.4; DB 22; Length 2984;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 1897; Conservative 0; Mismatches 12; Indels 7; Gaps 5;  
Qy 1 AATGATATGCCAACTTAAGTATTTACAGGGTGGCCCAATAGAACAGATGCACTCGCTG 60  
Db 1067 AATGATATGCCAACTTAAGTATTTACAGGGTGGCCCAATAGAACAGATGCACTCGCTG 1126  
Qy 61 TGATTTTAAGACAAGCTGTATTAACAGAACTCCACTGCAAGAGGGGCGCGGCGCAGGA 120  
Db 1127 TGATTTTAAGACAAGCTGTATTAACAGAACTCCACTGCAAGAGGGGCGCGGCGCAGGA 1186  
Qy 121 GAATCTCGCTGTGTCACAGAGAGGGGCTTAAGAGGGTCTCCACACTGCTGTAGGGCT 180  
Db 1187 GAATCTCGCTGTGTCACAGAGAGGGGCTTAAGAGGGTCTCCACACTGCTGTAGGGCT 1246  
Qy 181 GTTGCAATTTTATTAGTAGAAAGTGGAAAGGCTCTTCTCAACTTTTTCCTTGGGC 240  
Db 1247 GTTGCAATTTTATTAGTAGAAAGTGGAAAGGCTCTTCTCAACTTTTTCCTTGGGC 1306  
Qy 241 TGGAGAAATTAAGATCAGAAAGTTTCTGGAGTTTTCAGGCTATCATATATATCTATCT 300  
Db 1307 TGGAGAAATTAAGATCAGAAAGTTTCTGGAGTTTTCAGGCTATCATATATATCTATCT 1366  
Qy 301 GAAAGGCAACATATCTCTTCTCCCTCTTTTAAATTTTGTGTTCTTTCAGGCA 360  
Db 1367 GAAAGGCAACATATCTCTTCTCCCTCTTTTAAATTTTGTGTTCTTTCAGGCA 1426





PR 02-OCT-2000; 2000US-0679426.  
 PR 10-OCT-2000; 2000US-0685166.  
 XX (XUJ)/ XU J.  
 PA (DILL/) DILLON D C.  
 PA (MITC/) MITCHAM J L.  
 PA (HARL/) HARLOCKER S L.  
 PA (JIAN/) JIANG Y.  
 PA (KALO/) KALOS M D.  
 PA (FANG/) FANGER G R.  
 PA (RETT/) RETTER M W.  
 PA (STOL/) STOLK J A.  
 PA (DAYC/) DAY C H.  
 PA (VEDV/) VEDVICK T S.  
 PA (CART/) CARTER D.  
 PA (LISX/) LI S X.  
 PA (WANG/) WANG A.  
 PA (SKEI/) SKEIKY Y A W.  
 PA (HEPL/) HEPLER W T.  
 PA (HEND/) HENDERSON R A.  
 XX  
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;  
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS,  
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;  
 XX WPI; 2002-255649/30.  
 DR  
 XX New prostate-specific polynucleotides for diagnosing and treating  
 PT diseases, in particular prostate cancer, and as markers for the  
 PT progression of cancer -  
 XX  
 PS Claim 1; SEQ ID NO(335; 47pp; English.  
 XX  
 CC The present invention provides prostate-specific coding sequences and  
 CC their encoded proteins. These can be used in the diagnosis and treatment  
 CC of cancers, particularly prostate cancer. The present sequence is a cDNA  
 CC described in the invention.  
 XX  
 SQ Sequence 2984 BP; 837 A; 659 C; 645 G; 842 T; 1 other;  
 XX  
 Query Match 94.9%; Score 1836.4; DB 24; Length 2984;  
 Best Local Similarity 99.0%; Pred. No. 0;  
 Matches 1897; Conservative 0; Mismatches 12; Indels 7; Gaps 5;  
 QY 1 AATGGTATGCCAACTTAAGTATTACAGGCTGGCCCAATAGAACAGATGCACCTCGCTG 60  
 DB 1067 AATGGTATGCCAACTTAAGTATTACAGGCTGGCCCAATAGAACAGATGCACCTCGCTG 1126  
 QY 61 TGATTTTAAGACAGCTGTATAACAGAACTCCACTGCAAGAGGGGGCCGGGCCAGGA 120  
 DB 1127 TGATTTTAAGACAGCTGTATAACAGAACTCCACTGCAAGAGGGGGCCGGGCCAGGA 1186  
 QY 121 GAATCTCCGCTTGCCAGACAGGGGCCCTAAGAGGGTCTCCACACTGCTGTAGGGGCT 180  
 DB 1187 GAATCTCCGCTTGCCAGACAGGGGCCCTAAGAGGGTCTCCACACTGCTGTAGGGGCT 1246  
 QY 181 GTTGCAATTTTATTAGTAGAAGTGGAAAGCGCTCTTCTCAACTTTTTTCCCTTGGGC 240  
 DB 1247 GTTGCAATTTTATTAGTAGAAGTGGAAAGCGCTCTTCTCAACTTTTTTCCCTTGGGC 1306  
 QY 241 TCGAGAATTTAGAAATCAGAAATTTCTCGGAGTTTTCAGGCTATCATATATCTGTATCT 300  
 DB 1307 TCGAGAATTTAGAAATCAGAAATTTCTCGGAGTTTTCAGGCTATCATATATCTGTATCT 1366  
 QY 301 GAAAGCAACATAATTTCTTCCCTCCCTTTTAAATTTTGTGTTCTTTTTCAGCA 360  
 DB 1367 GAAAGCAACATAATTTCTTCCCTCCCTTTTAAATTTTGTGTTCTTTTTCAGCA 1426  
 QY 361 TTACTCACTAAAGGGCTCATTTTATGTCAGATTTTATGTCGGCTGCACCTTAACCTATG 420  
 DB 1427 TTACTCACTAAAGGGCTCATTTTATGTCAGATTTTATGTCGGCTGCACCTTAACCTATG 1486  
 QY 421 CCTCGCTTATTAGCCCGAGATCTGGTCTTTTNTGNTTTTTTTTTTTTTCGCTCTCCC 480

1487 CCTCGCTTATTAGCCCGAGATCTGGTCTTTT---TTTTTTTTTTTTTTCGCTCTCCC 1544  
 QY 481 CAAAGCTTTATCTGCTTCTGACCTTTTAAAAAGTTTGGGGGAGATTTCTGAATTTGGGCTA 540  
 DB 1545 CAAAGCTTTATCTGCTTCTGACCTTTTAAAAAGTTTGGGGGAGATTTCTGAATTTGGCTA 1603  
 QY 541 AAAGACATGCATTTTAAAACTAGGCAACTTCTTATTTCTTCTTTAAAAATACATAGC 600  
 DB 1604 AAAGACATGCATTTTAAAACTAG--CRACTCTTATTTCTTCTTTAAAAATACATAGC 1661  
 QY 601 ATTAAATCCAAATCTTATTAAAGACCTGACAGCTTGAAGAGTCACTACTGCAATTTAT 660  
 DB 1662 ATTAAATCCAAATCTTATTAAAGACCTGACAGCTTGAAGAGTCACTACTGCAATTTAT 1721  
 QY 661 AGGACCTTCTGCTGGTCTGCTGTTTCAAGTCTGCACAATCTTCTGAGAAATCTTTGC 720  
 DB 1722 AGGACCTTCTGCTGGTCTGCTGTTTCAAGTCTGCACAATCTTCTGAGAAATCTTTGC 1781  
 QY 721 ATGACAGAGAGGTAAGAGGTATTGGATTTTTCACAGAGGAAGAACACAGCGCAGAAATGAAG 780  
 DB 1782 ATGACAGAGAGGTAAGAGGTATTGGATTTTTCACAGAGGAAGAACACAGCGCAGAAATGAAG 1841  
 QY 781 GGCCAGGCTTACTGAGGCTGTCCAGTGGAGGCTCATGGGTGGGACATCGAAAAAGAGGC 840  
 DB 1842 GGCCAGGCTTACTGA-GCTGTCCAGTGGAGGCTCATGGGTGGGACATCGAAAAAGAGGC 1900  
 QY 841 AGCCTAGGCCCTGGGGAGGCCAGTCCACTGACAGCAAGGAGGACTGAGTGAGGCTTTTGC 900  
 DB 1901 AGCCTAGGCCCTGGGGAGGCCAGTCCACTGACAGCAAGGAGGACTGAGTGAGGCTTTTGC 1960  
 QY 901 AGGAAAAGGCTAAGAAAAAGGAAACCAATTTTAAACACAAAGAAACTGTCCAAATGC 960  
 DB 1961 AGGAAAAGGCTAAGAAAAAGGAAACCAATTTTAAACACAAAGAAACTGTCCAAATGC 2020  
 QY 961 TTTGGGAACGTGTTTATTGCTTATAATGGGTGCCCAAAATGGGTHAACCTAGACTTCAGA 1020  
 DB 2021 TTTGGGAACGTGTTTATTGCTTATAATGGGTGCCCAAAATGGGTHAACCTAGACTTCAGA 2080  
 QY 1021 GAGAATGACAGAGCAAGAGGAGAAATCTGCTGTCTTCCATTTTCAATTTCTGTTATCT 1080  
 DB 2081 GAGAATGACAGAGCAAGAGGAGAAATCTGCTGTCTTCCATTTTCAATTTCTGTTATCT 2140  
 QY 1081 CAGGTGAGCTGTAGAGGGGAGACATTAGAAAAAAATGAAAAACAAACAAATTTACTAAT 1140  
 DB 2141 CAGGTGAGCTGTAGAGGGGAGACATTAGAAAAAAATGAAAAACAAACAAATTTACTAAT 2200  
 QY 1141 GAGGTACGCTGAGGCTGGGAGTCTCTTGACTCCACTACTTAATTCGGTTTGTAGTGA 1200  
 DB 2201 GAGGTACGCTGAGGCTGGGAGTCTCTTGACTCCACTACTTAATTCGGTTTGTAGTGA 2260  
 QY 1201 CCTTTCAATTTTCTTTTATTAGAAGGGCAGCTTACTGTTGGTGGCAAAATTTGCCAACAT 1260  
 DB 2261 CCTTTCAATTTTCTTTTATTAGAAGGGCAGCTTACTGTTGGTGGCAAAATTTGCCAACAT 2320  
 QY 1261 AAGTTAAATAGAAAGTTGGCCAAATTTTCAACCCATTTTCTGCTGTTGGGCTCCACATTGCA 1320  
 DB 2321 AAGTTAAATAGAAAGTTGGCCAAATTTTCAACCCATTTTCTGCTGTTGGGCTCCACATTGCA 2380  
 QY 1321 ATGTTCAATGCAAGCTGTGCTGACACCGA CCGAGTACTAGCCAGCA CAAAGGCGAGG 1380  
 DB 2381 ATGTTCAATGCAAGCTGTGCTGACACCGA CCGAGTACTAGCCAGCA CAAAGGCGAGG 2440  
 QY 1381 TAGCCTGAATTCCTTCTGCTCTTTTACATTTCTTTTAAATAGCAATTTAGTGTCTCAGTC 1440  
 DB 2441 TAGCCTGAATTCCTTCTGCTCTTTTACATTTCTTTTAAATAGCAATTTAGTGTCTCAGTC 2500  
 QY 1441 CCTACTGAGTACTCTTTCTCTCCCTCTCTCAATTTTAAATTTCTTCAACTTGCATTTGC 1500  
 DB 2501 CCTACTGAGTACTCTTTCTCTCCCTCTCTCAATTTTAAATTTCTTCAACTTGCATTTGC 2560  
 QY 1501 AAGGATTACAAATTTCACTGTGATGTATTTGTTGCAAGNAGAAAGAAAAAGTGTCTT 1560

Db 2561 AAGATTACAACTTCACTGTGTATATGTTGCA-AAAAAAAAAAGTCTCTT 2619  
 QY 1561 TGTTTAAATTTACTTGTGTTGTAATCACTTGTCTTTTCCCATTTGAACCTAGTCAAT 1620  
 Db 2620 TGTTTAAATTTACTTGTGTTGTAATCACTTGTCTTTTCCCATTTGAACCTAGTCAAT 2679  
 QY 1621 AACCATCTCTGAACCTGTGTAAGAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGG 1680  
 Db 2680 AACCATCTCTGAACCTGTGTAAGAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGG 2739  
 QY 1681 TGAATTCGATGTTCTCAGAACCATTTCCACCCAGCAGCTGTTCTATCTGTTTAAATA 1740  
 Db 2740 TGAATTCGATGTTCTCAGAACCATTTCCACCCAGCAGCTGTTCTATCTGTTTAAATA 2799  
 QY 1741 AATTAGTTTGGGTTCTCTACATGCAATAACAAACCTGCTCCCAATCTGTCACATAAAGTC 1800  
 Db 2800 AATTAGTTTGGGTTCTCTACATGCAATAACAAACCTGCTCCCAATCTGTCACATAAAGTC 2859  
 QY 1801 TGTGACTTGAAGTTTGTAGTCAGCACCCCAACCAACTTTTATTTCTATGTTTGTGCA 1860  
 Db 2860 TGTGACTTGAAGTTTGTAGTCAGCACCCCAACCAACTTTTATTTCTATGTTTGTGCA 2919  
 QY 1861 ACATATGAGTGTGTTTGAAATAAAGTACCCATGCTCTTTTAAATAAATAAATAA 1916  
 Db 2920 ACATATGAGTGTGTTTGAAATAAAGTACCCATGCTCTTTTAAATAAATAAATAA 2975

RESULT 9  
 ACA59581  
 ID ACA59581 standard; cDNA; 2984 BP.  
 AC ACA59581;  
 XX  
 DT 10-JUN-2003 (first entry)  
 XX  
 DE Prostate cancer therapy associated cDNA #324.  
 KW Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;  
 KW immunogen; cancer; prostate specific antigen; PSA;  
 KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;  
 KW PSMA; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002192763-A1.  
 XX  
 PD 19-DEC-2002.  
 XX  
 PF 29-JUN-2001; 2001US-0895793.  
 XX  
 PR 17-APR-2000; 2000US-157455P.  
 PR 04-OCT-2000; 2000US-0679272.  
 PR 28-MAR-2001; 2001US-0822827.  
 XX  
 PA (XUJ/) XU J.  
 PA (DILL/) DILLON D C.  
 PA (MITC/) MITCHAM J L.  
 PA (HARL/) HARLOCKER S L.  
 PA (JIAN/) JIANG Y.  
 PA (KALO/) KALOS M D.  
 PA (FANG/) FANGER G R.  
 PA (RETT/) RETTER M W.  
 PA (DAYC/) DAY C H.  
 PA (VEDV/) VEDVICK T S.  
 PA (CART/) CARTER D.  
 PA (LISX/) LI S X.  
 PA (WANG/) WANG A.  
 PA (SKEI/) SKEIKY Y A W.  
 PA (HEPL/) HEPLER W T.  
 PA (HEND/) HENDERSON R A.  
 PA (HURA/) HURAL J.  
 PA (MCNE/) MCNEILL P D.

(HOUG/) HOUGHTON R L.  
 (DBAS/) Y DE BASSOLS C V.  
 (FOYT/) FOY T M.  
 Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;  
 Fanger GR, Retter MW, Stolk JA, Day CH, Vedwick TS, Carter D;  
 Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;  
 Mcneill PD, Houghton RL, Y De Bassols CV, Foy TM;  
 WPI; 2003-352711/33.  
 P-PSDB; ABU71662.  
 New fusion protein comprising prostate-specific polypeptides, or its  
 immunogenic portions, useful for diagnosing, preventing and/or treating  
 cancer, particularly prostate cancer -  
 Example 3; SEQ ID NO 335; 85pp; English.  
 The invention describes a fusion protein comprising at least one amino  
 acid sequence of immunogenic portions of any of the 3 sequences not  
 defined in the specification, or sequences having at least 70 or 90 %  
 sequence identity to any one of the 3 sequences defined in the USPTO  
 web site, which is encoded by any of the 4 nucleotide sequences not  
 defined in the specification. The fusion protein, composition and  
 methods are useful for diagnosing, preventing and/or treating cancer,  
 particularly prostate cancer. The proteins are useful as markers to  
 indicate the presence or absence of cancer. This sequence  
 represents a prostate cancer therapy associated cDNA.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from the US patent office at  
 CC seqdata.uspto.gov/sequence.html?docID=US20020192763.  
 XX  
 SQ. Sequence 2984 BP; 837 A; 659 C; 645 G; 842 T; 1 other;  
 Query Match 94.9%; Score 1836.4; DB 25; Length 2984;  
 Best Local Similarity 99.0%; Pred. No. 0;  
 Matches 1897; Conservative 0; Mismatches 12; Indels 7; Gaps 5;  
 QY 1 AANTGGTATGCCAACTTAAGTATTTACAGGTGGCCCAATAAGATGCACTCGCTG 60  
 Db 1067 AATGGTATGCCAACTTAAGTATTTACAGGTGGCCCAATAAGATGCACTCGCTG 1126  
 QY 61 TGATTTTAAAGCAAGCTGTATAACAGAACTCCACTGCAAGAGGNGGGCCGCCAGGA 120  
 Db 1127 TGATTTTAAAGCAAGCTGTATAACAGAACTCCACTGCAAGAGGNGGGCCGCCAGGA 1186  
 QY 121 GAATCTCCGCTTGTCCAAGACAGGGGCTTAAGGAGGCTCTCCACACTGCTGTAGGGCT 180  
 Db 1187 GAATCTCCGCTTGTCCAAGACAGGGGCTTAAGGAGGCTCTCCACACTGCTGTAGGGCT 1246  
 QY 181 GTTGCATTTTATTTAGTAGAAGTGGAAAGCCCTCTCTCAACTTTTCCCTTTGGGC 240  
 Db 1247 GTTGCATTTTATTTAGTAGAAGTGGAAAGCCCTCTCTCAACTTTTCCCTTTGGGC 1306  
 QY 241 TGGAGATTTTAGAATCAGAAGTTTCTCTGGAGTTTTCAGGCTATCATATATCTATCTCT 300  
 Db 1307 TGGAGATTTTAGAATCAGAAGTTTCTCTGGAGTTTTCAGGCTATCATATATCTATCTCT 1366  
 QY 301 GAAAGGCAACATAATTTCTTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360  
 Db 1367 GAAAGGCAACATAATTTCTTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1426  
 QY 361 TTAATCACTAAAGGGCTTCATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420  
 Db 1427 TTAATCACTAAAGGGCTTCATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1486  
 QY 421 CCTCGCTTATTTAGCCCGAGATCTGCTCTTTTNGTNTTTTNTTTTNTTTCGCTCTCC 480  
 Db 1487 CCTCGCTTATTTAGCCCGAGATCTGCTCTTTTNTT - TTTTNTTTCGCTCTCC 1544  
 QY 481 CAAAGCTTTATCTGCTCTGACATTTTAAAGAGTTTGGGGCAGATTTCTGAATGGGCTA 540



Db 1545 CAAAGCTTTATCTGTCTTGACTTTTAAAAAGTTTGGGGCAGATTCTGAATT-GGCTA 1603  
Qy 541 AAAGACATGCAATTTTAAAACTAGGCAACTTCTATTTCTTTCTTTTAAAAATACATAGC 600  
Db 1604 AAAGACATGCAATTTTAAAACTAG--CAACTCTTATTTCTTTCTTTTAAAAATACATAGC 1661  
Qy 601 ATTAAATCCCAATCTTATTTAAAGACCTGACAGCTTGAGAGGTCACACTGCATTTAT 660  
Db 1662 ATTAAATCCCAATCTTATTTAAAGACCTGACAGCTTGAGAGGTCACACTGCATTTAT 1721  
Qy 661 AGGACCTTCTGGTGGTCTCTGCTGTGTACGTTTGAAGTCTGACAATCCTTGAGAACTTTTC 720  
Db 1722 AGGACCTTCTGGTGGTCTCTGCTGTGTACGTTTGAAGTCTGACAATCCTTGAGAACTTTTC 1781  
Qy 721 ATGCAGAGGAGTGAAGAGTATTTGATTTTTCACAGAGGAAGAACACAGCGCAGAAATGAAG 780  
Db 1782 ATGCAGAGGAGTGAAGAGTATTTGATTTTTCACAGAGGAAGAACACAGCGCAGAAATGAAG 1841  
Qy 781 GGCCAGGCTTACTGAGGCTGTCCAGTGGAGGGCTCATGGTGGGACATGGAAAAAGAGGC 840  
Db 1842 GGCCAGGCTTACTGA-GCTGTCCAGTGGAGGGCTCATGGTGGGACATGGAAAAAGAGGC 1900  
Qy 841 AGCTTAGGCCCTGGGAGGCCAGTCCACTGAGCAAGCAAGGGACTGAGTGAGCCTTTTTC 900  
Db 1901 AGCTTAGGCCCTGGGAGGCCAGTCCACTGAGCAAGCAAGGGACTGAGTGAGCCTTTTTC 1960  
Qy 901 AGGAAAGGCTTAAGAAAAAGAAAAAACCATTCTAAAAACAAACAGAAACCTGTCCAAATGC 960  
Db 1961 AGGAAAGGCTTAAGAAAAAGAAAAAACCATTCTAAAAACAAACAGAAACCTGTCCAAATGC 2020  
Qy 961 TTTGGGAACGTGTTTATGTCCTATTAATGGGTCCCAAAATGGTAACTAGACTTCAGA 1020  
Db 2021 TTTGGGAACGTGTTTATGTCCTATTAATGGGTCCCAAAATGGTAACTAGACTTCAGA 2080  
Qy 1021 GAGAATGAGCAGAGCAAGAGGAGAACTCTGGTCTCCTTCCATTTCATTCGTGTATCT 1080  
Db 2081 GAGAATGAGCAGAGCAAGAGGAGAACTCTGGTCTCCTTCCATTTCATTCGTGTATCT 2140  
Qy 1081 CAGGTGAGCTGTGAGGGGAGAGCATTAGAAAAAAATGAAAAACAAACAAATTAATAAT 1140  
Db 2141 CAGGTGAGCTGTGAGGGGAGAGCATTAGAAAAAAATGAAAAACAAACAAATTAATAAT 2200  
Qy 1141 GAGGTAGCTGAGGCTGGAGTCTCTGACTCCACTACTTAATTCGGTTTAGTGAGAA 1200  
Db 2201 GAGGTAGCTGAGGCTGGAGTCTCTGACTCCACTACTTAATTCGGTTTAGTGAGAA 2260  
Qy 1201 CCTTCAATTTCTTTTATTAAGAGGCGAGCTTACTGTGTGGTGGCAAAATTCGCAACAT 1260  
Db 2261 CCTTCAATTTCTTTTATTAAGAGGCGAGCTTACTGTGTGGTGGCAAAATTCGCAACAT 2320  
Qy 1261 AAGTTAATAGAAAGTTGGCCAAATTTCAACCCCATTTTCTGTGGTTTGGGCTCCACATTGCA 1320  
Db 2321 AAGTTAATAGAAAGTTGGCCAAATTTCAACCCCATTTTCTGTGGTTTGGGCTCCACATTGCA 2380  
Qy 1321 ATGTTCAATGCCAGTGTGCTGACACCGACGGAGTACTAGCCAGCAAAAAGGCGAGG 1380  
Db 2381 ATGTTCAATGCCAGTGTGCTGACACCGACGGAGTACTAGCCAGCAAAAAGGCGAGG 2440  
Qy 1381 TAGCCTGAATGCTTCTGCTCTTTTACATTTCTTTTAAATAGCAATTTAGTGTCTCAGTC 1440  
Db 2441 TAGCCTGAATGCTTCTGCTCTTTTACATTTCTTTTAAATAGCAATTTAGTGTCTCAGTC 2500  
Qy 1441 CCTACTGAGTACTCTTCTCTCCCTCCTCTGAAATTAATTTCTTCAACTTGAATTTTC 1500  
Db 2501 CCTACTGAGTACTCTTCTCTCCCTCCTCTGAAATTAATTTCTTCAACTTGAATTTTC 2560  
Qy 1501 AAGGATTACATTTCACTGTGATGATATGTTGTCAGNAGAAAAAGAAAGTGTCTT 1560  
Db 2561 AAGGATTACATTTCACTGTGATGATATGTTGTTGCA-AAAAAAGAAAGTGTCTT 2619  
Qy 1561 TGTTTAAATTAATGTTGGTTGGAATCCATCTGCTTTTCCCATGGAAGTGTCTT 1620  
Db 2620 TGTTTAAATTAATGTTGGTTGGAATCCATCTGCTTTTCCCATGGAAGTGTCTT 2679

Qy 1621 AACCCATCTCTGAACCTGGTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTGCAGG 1680  
Db 2680 AACCCATCTCTGAACCTGGTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTGCAGG 2739  
Qy 1681 TGAATTTGGATGTTCTCAGAACCATTTACCCAGACAGCCTGTTCTATCTCTGTTTAATA 1740  
Db 2740 TGAATTTGGATGTTCTCAGAACCATTTACCCAGACAGCCTGTTCTATCTCTGTTTAATA 2799  
Qy 1741 AATTAGTTTGGGTTCTCTACATGATCAACAAACCCCTGCTCCAATCTGTCAATAAAAGTC 1800  
Db 2800 AATTAGTTTGGGTTCTCTACATGATCAACAAACCCCTGCTCCAATCTGTCAATAAAAGTC 2859  
Qy 1801 TGTGACTTGAAGTTTAGTTCAGCACCCCAACCAAACTTTATTTTCTATGTGTTTTCGA 1860  
Db 2860 TGTGACTTGAAGTTTAGTTCAGCACCCCAACCAAACTTTATTTTCTATGTGTTTTCGA 2919  
Qy 1861 ACATATGAGTGTGTTTGAATAATAAGTACCATGTCTTTATTAATAAANAANAANA 1916  
Db 2920 ACATATGAGTGTGTTTGAATAATAAGTACCATGTCTTTATTAATAAANAANAANA 2975

RESULT 10  
ABV25139 standard; cDNA; 3227 BP.  
XX AC ABV25139;  
XX AC  
DT 16-SEP-2002 (first entry)  
XX Human prostate expression marker cDNA 25130.  
DE Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
KW pharmacogenomic marker; gene; ss.  
XX Homo sapiens.  
XX WO200160860-A2.  
XX 23-AUG-2001.  
XX 20-FEB-2001; 2001WO-US05171.  
XX 17-FEB-2000; 2000US-183319P.  
PR 16-MAR-2000; 2000US-189862P.  
PR 25-MAY-2000; 2000US-207454P.  
PR 09-JUN-2000; 2000US-211314P.  
PR 18-JUL-2000; 2000US-219007P.  
PR 13-DEC-2000; 2000US-255281P.  
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX Schlegel R, Endege WO, Monahan JE;  
XX WPI; 2001-662795/76.  
DR Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -  
XX Claim 1; Page 4902; 11750pp; English.  
XX The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:  
CC (a) assessing whether a patient is afflicted with prostate cancer;  
CC (b) monitoring the progression of prostate cancer in a patient;  
CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;  
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound;

CC (g) determining whether prostate cancer has metastasized in a patient;  
CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
CC patient;  
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.  
XX Sequence 3227 BP; 879 A; 740 C; 765 G; 828 T; 15 other;  
SQ

Query Match 83.9%; Score 1624.6; DB 23; Length 3227;  
Best Local Similarity 92.4%; Pred. No. 0;  
Matches 1752; Conservative 0; Mismatches 134; Indels 10; Gaps 4;

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DB |||||  
QY 61 TGAATTTAAGACAAGCTGTATAAACAAGACTCCACTGCAAGAGGNGGCGCGGCAGGA 120  
DB |||||  
QY 1382 TGAATTTAAGACAAGCTGTATAAACAAGACTCCACTGCAAGAGGAGGCGCGGCAGGA 1441  
DB |||||  
QY 121 GAATCTCCGCTGTGTCACAGACAGGGGCTTAAGAGGGTCTCCACACTGCTGTAGGGCT 180  
DB |||||  
QY 1442 GAATCTCCGCTGTGTCACAGACAGGGGCTTAAGAGGGTCTCCACACTGCTGTAGGGCT 1501  
DB |||||  
QY 181 GTTGCAATTTTTTATTAGTAGAAGTGGNAAGGCTCTTCAACTTTTTTCCCTTGGGC 240  
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QY 1502 GTTGCAATTTTTTATTAGTAGAAGTGGNAAGGCTCTTCAACTTTTTTCCCTTGGGC 1561  
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QY 301 GAAAGGCAACATAATCTTCTCTCCCTCTTTTAAATTTTGTGTTCTTTTGCAGCA 360  
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QY 1622 GAAAGGCAACATAATCTTCTCTCCCTCTTTTAAATTTTGTGTTCTTTTGCAGCA 1681  
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QY 361 TPACTCACTAAGGGCTTCATTTAGTCCAGATTTTGTGCTGCTGCTGCTGCTGCTGCT 420  
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QY 481 CAAAGCTTTATCTGCTTGTGCTTTTAAAGGTTTGGGGCAGATCTGCAATTTGGCTA 540  
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QY 1802 CAAAGCTTTATCTGCTGCTGCTTTTAAAGGTTTGGGGCAGATCTGCAATTTGGCTA 1860  
DB |||||  
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DB |||||  
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DB |||||  
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DB |||||  
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DB |||||  
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DB |||||  
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QY 2099 GGCAGGCTTCTGAG--GCTGTCCAGTGGAGGCTCATGGGTGGGACATGGAAGAAAGGC 2157  
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DB |||||  
QY 2158 AGCTAGGCGCTGGGAGCGCAGTCCACTGACAGAGGAGGAGTGAAGTGAAGCTTTTGC 2217  
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QY 901 AGGAAAGGCTTAAGAAAGGAAAAACCAATTTTAAACACAAAGAACTCTCCAAATGC 960  
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DB 2218 AGGAAAAGGCTAAGAAAAAGGAAAAACCATTTCTTAAAAACAAAGAACTGTCCAAATGC 2277  
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DB |||||  
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DB |||||  
QY 2518 CTTTCAATTTCTTTTATTAGAGGGCAGCTTACTGTGGTGCAAAATTTGCCAAT 2577  
DB |||||  
QY 1261 AAGTTAATAGAAAGTTGCCAATTTTCACTTAAATTTTCTGCTGTTGGCTCCCAATTGCA 1320  
DB |||||  
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DB |||||  
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QY 2878 CTTTCTTTTGTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 2937  
DB |||||  
QY 1615 GTCAATTAACCTCTCTGAACTGTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1674  
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DB |||||  
QY 3058 TAAATAAATAAATTTGGGGTGTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 3117  
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DB |||||  
QY 1855 TTTGCAACATATGAGT 1890  
DB |||||  
QY 3178 TTTGGCAACAAAAAGGGTGTGAAAAAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 3213  
DB |||||

RESULT 11  
ABV22893  
ID ABV22893 standard; cDNA; 3228 BP.  
XX AC ABV22893;  
XX

DT 13-SEP-2002 (first entry)  
 XX Human prostate expression marker cDNA 22884.  
 DE Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 KW pharmacogenomic marker; gene; ss.  
 KW Homo sapiens.  
 OS WO200160860-A2.  
 XX 23-AUG-2001.  
 XX 20-FEB-2001; 2001WO-US05171.  
 XX 17-FEB-2000; 2000US-183319P.  
 PR 16-MAR-2000; 2000US-189862P.  
 PR 25-MAY-2000; 2000US-207454P.  
 PR 09-JUN-2000; 2000US-211314P.  
 PR 18-JUL-2000; 2000US-219007P.  
 PR 13-DEC-2000; 2000US-255281P.  
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 PA Schlegel R, Endege WO, Monahan JE;  
 PI WPI; 2001-662795/76.  
 DR Novel isolated nucleic acid molecule associated with cancerous state of  
 XX prostate cells and correlating with presence of prostate cancer, useful  
 PT for detecting presence of prostate cancer, stage of prostate cancer -  
 PT Claim 1; Page 4055; 11750pp; English.  
 XX The invention relates to an isolated nucleic acid molecule (I) comprising  
 PS a nucleotide sequence given in Tables 1-9 (ASV0010-ABV62213) of the  
 XX specification or its complement. (I) is useful for:  
 CC (a) assessing whether a patient is afflicted with prostate cancer;  
 CC (b) monitoring the progression of prostate cancer in a patient;  
 CC (c) assessing the efficacy of a test compound to inhibit prostate  
 CC cancer in a patient;  
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
 CC in a patient;  
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound;  
 CC (g) determining whether prostate cancer has metastasized in a patient;  
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
 CC patient;  
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.  
 XX Sequence 3228 BP; 879 A; 740 C; 765 G; 829 T; 15 other;  
 SQ  
 Query Match 83.7%; Score 1620.6; DB 23; Length 3228;  
 Best Local Similarity 92.8%; Pred. No. 0;  
 Matches 1757; Conservative 0; Mismatches 129; Indels 12; Gaps 5;  
 QY 1 AATGGTATGCCAATCTTAAGTATTATACAGGTGGCCCAATAGAACAGATGCACTCGCTG 60  
 DB 1322 AATGGTATGCCAATCTTAAGTATTATACAGGTGGCCCAATAGAACAGATGCACTCGCTG 1381  
 QY 61 TGATTTTAAGACAAGCTGTATATAACAGAACTCCACTGCAAGAGGGGCGCCGCCAGGA 120  
 DB 1382 TGATTTTAAGACAAGCTGTATATAACAGAACTCCACTGCAAGAGGGGCGCCGCCAGGA 1441  
 QY 121 GAATCTCCGCTTGTCACAGACAGGGGCTTAAGAGGGTCTCCACACTGCTAGGGGCT 180  
 DB 1442 GAATCTCCGCTTGTCACAGACAGGGGCTTAAGAGGGTCTCCACACTGCTAGGGGCT 1501  
 QY 181 GTTGCAATTTTATTAGTAGAAGTGGAAAGGCTCTTCTCAACTTTTTCCTTGGGC 240  
 DB 1502 GTTGCAATTTTATTAGTAGAAGTGGAAAGGCTCTTCTCAACTTTTTCCTTGGGC 1561  
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 DB 1622 GAAAGCAACATAATTTCTTCCCTCTCTTAAATAATTTCTGTTTCTTTTTCAGCA 1681  
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GenCore version 5.1.6  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	1388.8	71.7	2051	4	US-09-328-475C-334
C 5	641.2	33.1	1024	4	US-09-328-475C-81
C 6	628.4	32.5	1024	4	US-09-328-475C-96
C 7	628.2	32.4	1024	4	US-09-328-475C-82
C 8	622	32.1	1024	4	US-09-328-475C-95
C 9	615.6	31.8	1013	4	US-09-328-475C-14
C 10	584.6	30.2	948	4	US-09-328-475C-23
C 11	582.2	30.1	720	4	US-09-328-475C-319
C 12	581	30.0	744	4	US-09-328-475C-318
C 13	539.6	27.9	980	4	US-09-328-475C-19
C 14	469.4	24.2	484	4	US-09-439-313-434
C 15	469.4	24.2	484	4	US-09-352-616A-434
C 16	421.6	21.8	1020	4	US-09-328-475C-102
C 17	421.6	21.8	1021	4	US-09-328-475C-103
C 18	411	21.2	822	4	US-09-328-475C-223
C 19	378.2	19.5	497	4	US-09-328-475C-222
C 20	350.4	18.1	366	3	US-09-020-956-115
C 21	350.4	18.1	366	3	US-09-030-607-115
C 22	350.4	18.1	366	4	US-09-439-313-115
C 23	350.4	18.1	366	4	US-09-352-616A-115
C 24	350.4	18.1	366	4	US-09-232-149A-115
C 25	332	17.1	335	3	US-09-020-956-141
C 26	332	17.1	335	3	US-09-030-607-141
C 27	332	17.1	335	4	US-09-439-313-141

C 28	332	17.1	335	4	US-09-352-616A-141	Sequence 141, App
C 29	332	17.1	335	4	US-09-232-149A-141	Sequence 141, App
C 30	332	16.7	323	3	US-09-020-956-128	Sequence 128, App
C 31	332	16.7	323	3	US-09-030-607-128	Sequence 128, App
C 32	332	16.7	323	3	US-09-439-313-128	Sequence 128, App
C 33	332	16.7	323	4	US-09-352-616A-128	Sequence 128, App
C 34	332	16.7	323	4	US-09-232-149A-128	Sequence 128, App
C 35	319.4	16.5	499	4	US-09-328-475C-185	Sequence 185, App
C 36	308.6	15.9	317	4	US-09-439-313-453	Sequence 453, App
C 37	308.6	15.9	317	4	US-09-352-616A-453	Sequence 453, App
C 38	288	14.9	305	4	US-09-439-313-295	Sequence 295, App
C 39	288	14.9	305	4	US-09-352-616A-295	Sequence 295, App
C 40	288	14.9	305	4	US-09-232-149A-295	Sequence 295, App
C 41	282.4	14.6	624	4	US-09-439-313-443	Sequence 443, App
C 42	282.4	14.6	624	4	US-09-352-616A-443	Sequence 443, App
C 43	268.8	13.9	332	3	US-09-030-607-207	Sequence 207, App
C 44	268.8	13.9	332	4	US-09-439-313-207	Sequence 207, App
C 45	268.8	13.9	332	4	US-09-352-616A-207	Sequence 207, App

ALIGNMENTS

RESULT 1  
US-09-439-313-335  
; Sequence 335, Application US/09439313  
; Patent No. 6329505  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan Louise  
; APPLICANT: Jiang Yuqui  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Kalos, Michael  
; APPLICANT: Fanger, Gary  
; APPLICANT: Retter, Mark  
; APPLICANT: Solk, John  
; APPLICANT: Day, Craig  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
; FILE REFERENCE: 210121.427C9  
; CURRENT APPLICATION NUMBER: US/09/439,313  
; CURRENT FILING DATE: 1999-11-12  
; NUMBER OF SEQ ID NOS: 575  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 335  
; LENGTH: 2984  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-439-313-335

Query Match	94.9%;	Score	1836.4;	DB	4;	Length	2984;
Best Local Similarity	99.0%;	Pred. No.	0;				
Mismatches	1897;	Conservative	0;	Mismatches	12;	Indels	7;
Gaps	5;						
QY	1	AATGTTATGCCAACTTAAGTATTTCACGGTGGCCCAATAGAACAAAGATGCACTCGCTG	60				
DB	1067	AATGTTATGCCAACTTAAGTATTTCACGGTGGCCCAATAGAACAAAGATGCACTCGCTG	1126				
QY	61	TGATTTTAAGACAAGCTGTATAACAGAACTCCACTGCAAGAGGNGGCGGGCCAGGA	120				
DB	1127	TGATTTTAAGACAAGCTGTATAACAGAACTCCACTGCAAGAGGNGGCGGGCCAGGA	1186				
QY	121	GAATCTCGCTGTTCACAGACAGGGGCTTAAGAGGGTCTCCACACTGCTGTAGGGGT	180				
DB	1187	GAATCTCGCTGTTCACAGACAGGGGCTTAAGAGGGTCTCCACACTGCTGTAGGGGT	1246				
QY	181	GTTCATTTTATTTATTAGTAGAAAGTGGAAAGGCTCTTCTCAACTTTTTTCCCTTGGGC	240				
DB	1247	GTTCATTTTATTTATTAGTAGAAAGTGGAAAGGCTCTTCTCAACTTTTTTCCCTTGGGC	1306				
QY	241	TGGAGATTTAGAAATCAGAAGTTTCTCGAGTTTTCAGGCTATCATATATCTGTATCT	300				











OTHER INFORMATION: n = A,T,C or G  
US-09-328-475C-81

Query Match  
Best Local Similarity 33.1%; Score 641.2; DB 4; Length 1024;  
Matches: 681; Conservative 0; Mismatches 16; Indels 3; Gaps 3;  
QY 448 CTTTNTGTTGTTTTTTTTTTTTTTTTTTTTTCCGCTCTCCCAAGCTTATCTGCTTGTACTTTTA 507  
Db CTTTNTGTTGTTTTTTTTTTTTTTTTTTTTTCCGCTCTCCCAAGCTTATCTGCTTGTACTTTTA 507  
QY 799 CTTTNTGTTGTTTTTTTTTTTTTTTTTTTTTCCGCTCTCCCAAGCTTATCTGCTTGTACTTTTA 740  
Db CTTTNTGTTGTTTTTTTTTTTTTTTTTTTTTCCGCTCTCCCAAGCTTATCTGCTTGTACTTTTA 740  
QY 508 AAAAGTTTGGGGGAGATCTGAATTTGGCTTAAAGACATGCAATTTTAAAGCTAGGCA 567  
Db AAAAGTTTGGGGGAGATCTGAATTTGGCTTAAAGACATGCAATTTTAAAGCTAGGCA 567  
QY 739 AAAAGTTTGGGGGAGATCTGAATTTGGCTTAAAGACATGCAATTTTAAAGCTAGGCA 682  
Db AAAAGTTTGGGGGAGATCTGAATTTGGCTTAAAGACATGCAATTTTAAAGCTAGGCA 682  
QY 568 ACTTCTTATTTCTTTTCTTTTAAATAATACATAGCAATTAATCCCAATCTTATTTAAAGAC 627  
Db ACTTCTTATTTCTTTTCTTTTAAATAATACATAGCAATTAATCCCAATCTTATTTAAAGAC 627  
QY 628 CTGACAGCTTGAGAGGCTCACTACTGCAATTTATAGGACCTTCTGGTGGTCTGCTGTAC 687  
Db CTGACAGCTTGAGAGGCTCACTACTGCAATTTATAGGACCTTCTGGTGGTCTGCTGTAC 687  
QY 621 CTGACAGCTTGAGAGGCTCACTACTGCAATTTATAGGACCTTCTGGTGGTCTGCTGTAC 562  
Db CTGACAGCTTGAGAGGCTCACTACTGCAATTTATAGGACCTTCTGGTGGTCTGCTGTAC 562  
QY 688 GTTGAAGTCTGACAACTCTTGAATCTTTGCAATGCAAGAGGTAAGAGGTATTTGGAT 747  
Db GTTGAAGTCTGACAACTCTTGAATCTTTGCAATGCAAGAGGTAAGAGGTATTTGGAT 747  
QY 561 GTTGAAGTCTGACAACTCTTGAATCTTTGCAATGCAAGAGGTAAGAGGTATTTGGAT 502  
Db GTTGAAGTCTGACAACTCTTGAATCTTTGCAATGCAAGAGGTAAGAGGTATTTGGAT 502  
QY 748 TTTTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 807  
Db TTTTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 807  
QY 501 TTTTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 443  
Db TTTTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 443  
QY 808 GAGGCTCATGTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 867  
Db GAGGCTCATGTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 867  
QY 442 GAGGCTCATGTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 383  
Db GAGGCTCATGTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 383  
QY 868 CTGAGCAAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 927  
Db CTGAGCAAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 927  
QY 382 CTGAGCAAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 323  
Db CTGAGCAAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 323  
QY 928 ATTCTAAACACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 987  
Db ATTCTAAACACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 987  
QY 322 ATTCTAAACACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 987  
Db ATTCTAAACACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 987  
QY 988 TGGGTCCTCCCAATGGTAACTAGACTTCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1047  
Db TGGGTCCTCCCAATGGTAACTAGACTTCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1047  
QY 262 TGGTCTCCCAATGGTAACTAGACTTCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 203  
Db TGGTCTCCCAATGGTAACTAGACTTCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 203  
QY 1048 TCTGCTGCT 1107  
Db TCTGCTGCT 1107  
QY 202 TCTGCTGCT 143  
Db TCTGCTGCT 143  
QY 1108 AGAAAAAATGAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1147  
Db AGAAAAAATGAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1147

RESULT 6  
US-09-328-475C-96/c  
Sequence 96, Application US/09328475C  
Patent No. 6476207  
GENERAL INFORMATION:  
APPLICANT: Zhang, Jimmy  
APPLICANT: Astel, Jon H.  
APPLICANT: Carroll III, Eddie  
APPLICANT: Endege, Wilson O.  
APPLICANT: Ford, Donna M.  
APPLICANT: Monahan, John E.  
APPLICANT: Schlegel, Robert  
APPLICANT: Steinmann, Kathleen P.  
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT  
ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER.  
FILE REFERENCE: 1532.002/200130.463  
CURRENT APPLICATION NUMBER: US/09/328,475C

CURRENT FILING DATE: 1999-06-09  
NUMBER OF SEQ ID NOS: 341  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 96  
LENGTH: 1024  
TYPE: DNA  
ORGANISM: Homo Sapien  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1) ... (1024)  
OTHER INFORMATION: n = A, T, C or G  
US-09-328-475C-96

Query Match  
Best Local Similarity 32.5%; Score 628.4; DB 4; Length 1024;  
Matches: 678; Conservative 0; Mismatches 13; Indels 5; Gaps 4;  
QY 453 TTTTNTGTTTNTTTTTTTTTTTTTTTTTTTTTTCCGCTCTCCCAAGCTTATCTGT-CITGACTTTTAAAAA 511  
Db TTTTNTGTTTNTTTTTTTTTTTTTTTTTTTTTTCCGCTCTCCCAAGCTTATCTGT-CITGACTTTTAAAAA 511  
QY 795 TTTTNTGTTTNTTTTTTTTTTTTTTTTTTTTTTCCGCTCTCCCAAGCTTATCTGT-CITGACTTTTAAAAA 736  
Db TTTTNTGTTTNTTTTTTTTTTTTTTTTTTTTTTCCGCTCTCCCAAGCTTATCTGT-CITGACTTTTAAAAA 736  
QY 512 AGTTTGGGGGAGATCTGAATTTGGCTTAAAGACATGCAATTTTAAAGCTAGGCACTT 571  
Db AGTTTGGGGGAGATCTGAATTTGGCTTAAAGACATGCAATTTTAAAGCTAGGCACTT 571  
QY 735 AGTTTGGGGGAGATCTGAATTTGGCTTAAAGACATGCAATTTTAAAGCTAGGCACTT 679  
Db AGTTTGGGGGAGATCTGAATTTGGCTTAAAGACATGCAATTTTAAAGCTAGGCACTT 679  
QY 572 CTTATTTCTTTCTTTTAAATAATACATAGCAATTAATCCCAATCTTATTTAAAGACTTCA 631  
Db CTTATTTCTTTCTTTTAAATAATACATAGCAATTAATCCCAATCTTATTTAAAGACTTCA 631  
QY 678 CTTATTTCTTTCTTTTAAATAATACATAGCAATTAATCCCAATCTTATTTAAAGACTTCA 619  
Db CTTATTTCTTTCTTTTAAATAATACATAGCAATTAATCCCAATCTTATTTAAAGACTTCA 619  
QY 632 CAGCTTGAGAGGCTCACTACTGCAATTTATAGGACCTTCTGGTGGTCTGCTGTAGTTT 691  
Db CAGCTTGAGAGGCTCACTACTGCAATTTATAGGACCTTCTGGTGGTCTGCTGTAGTTT 691  
QY 618 CAGCTTGAGAGGCTCACTACTGCAATTTATAGGACCTTCTGGTGGTCTGCTGTAGTTT 559  
Db CAGCTTGAGAGGCTCACTACTGCAATTTATAGGACCTTCTGGTGGTCTGCTGTAGTTT 559  
QY 692 GAACTCTGACAACTCTTGAATCTTGCATGCAAGAGGTAAGAGGTATTTGGATTTT 751  
Db GAACTCTGACAACTCTTGAATCTTGCATGCAAGAGGTAAGAGGTATTTGGATTTT 751  
QY 558 GAACTCTGACAACTCTTGAATCTTGCATGCAAGAGGTAAGAGGTATTTGGATTTT 499  
Db GAACTCTGACAACTCTTGAATCTTGCATGCAAGAGGTAAGAGGTATTTGGATTTT 499  
QY 752 ACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 811  
Db ACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 811  
QY 498 ACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 871  
Db ACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 871  
QY 812 GCTCATGGTGGGAGCATGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 439  
Db GCTCATGGTGGGAGCATGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 439  
QY 439 GCTCATGGTGGGAGCATGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 871  
Db GCTCATGGTGGGAGCATGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 871  
QY 872 GCAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 380  
Db GCAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 380  
QY 379 GCAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 931  
Db GCAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 931  
QY 932 TAAAAACACAAAGAGAACTGTCCAAATGCTTTGGGAACTGTGTTTATTCCTATAATGGG 991  
Db TAAAAACACAAAGAGAACTGTCCAAATGCTTTGGGAACTGTGTTTATTCCTATAATGGG 991  
QY 319 TAAAAACACAAAGAGAACTGTCCAAATGCTTTGGGAACTGTGTTTATTCCTATAATGGG 260  
Db TAAAAACACAAAGAGAACTGTCCAAATGCTTTGGGAACTGTGTTTATTCCTATAATGGG 260  
QY 992 TCCCAAAATGGGTAACTAGACTTCAGAGAGATGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 1051  
Db TCCCAAAATGGGTAACTAGACTTCAGAGAGATGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 1051  
QY 259 TCCCAAAATGGGTAACTAGACTTCAGAGAGATGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 200  
Db TCCCAAAATGGGTAACTAGACTTCAGAGAGATGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 200  
QY 1052 GCTGCTCTTCCATTTTCAATCTGTTATCTCAGGTGAGCTGTTAGAGGGAGGAGGAGGAGG 1111  
Db GCTGCTCTTCCATTTTCAATCTGTTATCTCAGGTGAGCTGTTAGAGGGAGGAGGAGGAGG 1111  
QY 199 GCTGCTCTTCCATTTTCAATCTGTTATCTCAGGTGAGCTGTTAGAGGGAGGAGGAGGAGG 140  
Db GCTGCTCTTCCATTTTCAATCTGTTATCTCAGGTGAGCTGTTAGAGGGAGGAGGAGGAGG 140  
QY 1112 AAAAATGAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1147  
Db AAAAATGAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1147

RESULT 7  
US-09-328-475C-82  
Sequence 82, Application US/09328475C  
Patent No. 6476207  
GENERAL INFORMATION:  
APPLICANT: Zhang, Jimmy  
APPLICANT: Astel, Jon H.

APPLICANT:	Carroll III, Eddie			
APPLICANT:	Endege, Wilson O.			
APPLICANT:	Ford, Donna M.			
APPLICANT:	Monahan, John E.			
APPLICANT:	Schlegel, Robert			
APPLICANT:	Steinmann, Kathleen E.			
TITLE OF INVENTION:	GENES AND GENE EXPRESSION PRODUCTS THAT ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER			
FILE REFERENCE:	1532.002/200130.463			
CURRENT APPLICATION NUMBER:	US/09/328.475C			
CURRENT FILING DATE:	1999-06-09			
NUMBER OF SEQ ID NOS:	341			
SOFTWARE:	FastSeq for Windows Version 3.0			
SEQ ID NO 82				
LENGTH:	1024			
TYPE:	DNA			
ORGANISM:	Homo Sapien			
FEATURE:				
NAME/KEY:	misc_feature			
LOCATION:	(1)...(1024)			
OTHER INFORMATION:	n = A,T,C or G			
US-09-328-475C-82				
Query Match	32.4%;	Score 628.2;	DB 4;	Length 1024;
Best Local Similarity	94.9%;	Pred. No. 1.5e-164;		
Matches 690;	Conservative 0;	Mismatches 32;	Indels 5;	Gaps 4;
Qy	422	CTCCCTTATTATAGCCCGAGATCTGGTCTTTTNTGNTTNTTTTTTTTTCGGTCTCCCC	481	
Db	75	CGCCCTTAGCGTGGTTCGGCGCGAGGTACTCTTTTTTTTTTTTTTTTTCGGTCTCCCC	134	
Qy	482	AAAGCTTTATCTGCTCTTGACTTTTTTAAAAAGTTTGGGGGAGATCTGAATTGGGCTAA	541	
Db	135	AAAGCTTTATCTGCTTGACTTTTTTAAAAAGTTTGGGGGAGATCTGAATT-GGCTAA	193	
Qy	542	AAGCATGTCATTTTAAACCTAGCACTCTTAATTTCTTTTAAAAATACATGACA	601	
Db	194	AAGCATGTCATTTTAAACCTAG--CAACTCTTAATTTCTTTTAAAAATACATGACA	251	
Qy	602	TTAAATCCCAATCCTATTTAAAGACCTGCAGCTTGAGAAGGTCACTTACGTCATTTATA	661	
Db	252	TTAAATCCCAATCCTATTTAAAGACCTGCAGCTTGAGAAGGTCACTTACGTCATTTATA	311	
Qy	662	GGACCTTCTGGTGGTTCTGCTGTTACGTTGAAGTCTGCACATCCTTGAGAACTCTTGCA	721	
Db	312	GGACCTTCTGGTGGTTCTGCTGTTACGTTGAAGTCTGCACATCCTTGAGAACTCTTGCA	371	
Qy	722	TGCAGAGAGGTAAAGAGTATTGATTTTTCACAGAGGAAGAACACAGCCAGAAATGAAG	781	
Db	372	TGCAGAGAGGTAAAGAGTATTGATTTTTCACAGAGGAAGAACACAGCCAGAAATGAAG	431	
Qy	782	GCCAGGCTTACTAGGGCTGTCACAGTGAGGGCTCATGGTGGGACATCGAAAGAGGCA	841	
Db	432	GCCAGGCTTACTGA-GCTGTCCAGTGAGGGCTCATGGTGGGACATCGAAAGAGGCA	490	
Qy	842	GCCTAGGCCCTGGGAGCCCACTGCAGTGCAGCAAGGACCTGAGTGAGCCCTTTTGCA	901	
Db	491	GCCTAGGCCCTGGGAGCCCACTGCAGTGCAGCAAGGACCTGAGTGAGCCCTTTTGCA	550	
Qy	902	GGAAAAGGCTAAGAAAAGGAAAACCAATTCTTAAACACACACAGAAACTGTGCCAAATGCT	961	
Db	551	GGAAAAGGCTAAGAAAAGGAAAACCAATTCTTAAACACACACAGAAACTGTGCCAAATGCT	610	
Qy	962	TTGGGAAGCTGTGTTTATTGCTTAATGGGTGCCCAAAATGGGTAAACCTAGACTTCAGAG	1021	
Db	611	TTGGGAAGCTGTGTTTATTGCTTAATGGGTGCCCAAAATGGGTAAACCTAGACTTCAGAG	670	
Qy	1022	AGAATGACGAGAGCAAGAGAGAAATCTGGCTGTCTTCCATTTTTCATTTCTGTATCTC	1081	
Db	571	AGAATGACGAGAGCAAGAGAGAAATCTGGCTGTCTTCCATTTTTCATTTCTGTATCTC	730	
Qy	1082	AGGTGAGCTGGTAGAGGGGAGACATTAGAAAAAATGAAACAA-CAAAAACAAATTAAT	1140	



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QY 508 AAAAAAGTTGGGGCAGATTCTGAAATGGGCTAAAGACATGCAATTTTAAACCTAGGCA 567
Db 62 AAAAAAGTTGGGGCAGATTCTGAAAT--GGCTAAAGACATGCAATTTTAAACCTAG--C 118
QY 568 ACTCTTATTTCTTTCTTTTAAATAATACATAGCAATTAATCCCAATCCTATTAAAGAC 627
Db 119 AACTCTTATTTCTTTCTTTTAAATAATACATAGCAATTAATCCCAATCCTATTAAAGAC 178
QY 628 CTGACAGCTTTGAGAAGGTCTACTGCAATTTATAGGACCTTTCTGGTGGTTCTGCTGTAC 687
Db 179 CTGACAGCTTTGAGAAGGTCTACTGCAATTTATAGGACCTTTCTGGTGGTTCTGCTGTAC 238
QY 688 GTTTGAAGTCTGCAATCTTTGCAATCTTTGCAATCTTTGCAATCTTTGCAATCTTTGCAAT 747
Db 239 GTTTGAAGTCTGCAATCTTTGCAATCTTTGCAATCTTTGCAATCTTTGCAATCTTTGCAAT 298
QY 748 TTTTACAGAGGAAGAACACAGCGCAGCAATGAAGGGCCAGGCTTACTGAGGCTGTCAGTG 807
Db 299 TTTTACAGAGGAAGAACACAGCGCAGCAATGAAGGGCCAGGCTTACTGAGGCTGTCAGTG 357
QY 808 GAGGGCTCATGGGTGGGACATGGAAAGAGAGGAGGCTTAGGGCCCTGGGGAGCCAGTCCA 867
Db 358 GAGGGCTCATGGGTGGGACATGGAAAGAGAGGAGGCTTAGGGCCCTGGGGAGCCAGTCCA 417
QY 868 CTGAGCAGCAAGGACTGAGTGAAGCTTTTGCAGGAAAGGCTTAAGAAAAAGGAAAAACC 927
Db 418 CTGAGCAGCAAGGACTGAGTGAAGCTTTTGCAGGAAAGGCTTAAGAAAAAGGAAAAACC 477
QY 928 ATTCTTAAACACACAAAGAACTGTCCAAATGCTTTTGGGAAGCTGTGTTATTCCTTAA 987
Db 478 ATTCTTAAACACACAAAGAACTGTCCAAATGCTTTTGGGAAGCTGTGTTATTCCTTAA 537
QY 988 TGGGTCCCCAAAATGGGTAACTTAGACTTCAGAGAGAAATGAGCAGAG--AGCAAAGGAGAA 1046
Db 538 TGGGTCCCCAAAATGGGTAACTTAGACTTCAGAGAGAAATGAGCAGAGAGGAGAA 597
QY 1047 ATCT--GGCTGCTCTTCAATTTTCAATCTGTTATC--TCAGGTGAGCTGGT--AGAGGGAG 1102
Db 598 ATCTGGGCTGCTCTTCAATTTTCAATCTGTTATC--TCAGGTGAGCTGGT--AGAGGGAG 657
QY 1103 ACATTAG--AAAAAATGAACAAACAAACAACTTACTAATGAGGTAC 1147
Db 658 ACATTAGAAAAAATGAACAAACAAACAACTTACTAATGAGGTAC 703
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## RESULT 11

```
US-09-328-475C-319/c
; Sequence 319, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 319
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(720)
; OTHER INFORMATION: n = A,T,C or G
```

## US-09-328-475C-319

```
Query Match 30.1%; Score 582.2; DB 4; Length 720;
Best Local Similarity 97.6%; Pred. No. 7.4e-152;
Matches 622; Conservative 0; Mismatches 10; Indels 5; Gaps 3;
QY 511 AAGTTGGGGCAGATTCTGAAATGGGCTAAAGACATGCAATTTTAAACCTAGGCACT 570
Db 720 AAGTTGGGGCAGATTCTGAAAT--GGTTAAAGACATGCAATTTTAAACCTAGCAACTC 662
QY 571 TCTTATTTCTTTCTTTTAAATAATACATAGCAATTAATCCCAATCCTATTAAAGACCTG 630
Db 661 ----TATTTCTTTCTTTTAAATAATACATAGCAATTAATCCCAATCCTATTAAAGCCTG 605
QY 631 ACAGCTTGAGAAGGTCACTACTGCAATTTATAGGACCTTCTGGTGGTTCTGCTGTACGTT 690
Db 604 ACAGCTTGAGAAGGTCACTACTGCAATTTATAGGACCTTCTGGTGGTTCTGCTGTACGTT 545
QY 691 TGAAGTCTGCAATCTTTGAGAAATCTTTGCAATCTGAGAGGAGTAAGAGGTATTGATTTT 750
Db 544 TGAAGTCTGCAATCTTTGAGAAATCTTTGCAATCTGAGAGGAGTAAGAGGTATTGATTTT 485
QY 751 CACAGAGGAAGAACACAGCGCAGCAATGAAGGGCCAGGCTTACTGAGGCTGTCAGTGGAG 810
Db 484 CACAGAGGAAGAACACAGCGCAGCAATGAAGGGCCAGGCTTACTGAG--GCTGTCCAGTGGAG 426
QY 811 GGCTCATGTTGGGACATGGAAGAGAGGAGGAGGCTTAGGGCCCTGGGGAGGCCAGTCCACTG 870
Db 425 GGCTCATGTTGGGACATGGAAGAGAGGAGGAGGCTTAGGGCCCTGGGGAGGCCAGTCCACTG 366
QY 871 AGCAAGCAAGGACTGAGTGAAGCTTTTGCAGGAAAGGCTAAGAAAAAGGAAAAACCAAT 930
Db 365 AGCAAGCAAGGACTGAGTGAAGCTTTTGCAGGAAAGGCTAAGAAAAAGGAAAAACCAAT 306
QY 931 CTAAACACAAACAGAAAGTGTCCAAATGCTTTGGGAAGCTGTGTTATTCCTTAATGG 990
Db 305 CTAAACACAAACAGAAAGTGTCCAAATGCTTTGGGAAGCTGTGTTATTCCTTAATGG 246
QY 991 GTCCCCAAAATGGGTAACTTAGACTTCAGAGAGAAATGAGCAGAGAGCAAGAGAAATCT 1050
Db 245 GTCCCCAAAATGGGTAACTTAGACTTCAGAGAGAAATGAGCAGAGAGCAAGAGAAATCT 186
QY 1051 GGCTGCTCTTCAATTTTCAATCTGTTATCTAGGTGAGCTGAGTGGGAGGAGCAATTAGA 1110
Db 185 GGCTGCTCTTCAATTTTCAATCTGTTATCTAGGTGAGCTGAGTGGGAGGAGCAATTAGA 126
QY 1111 AAAAAATGAACAAACAAACAACTTACTAATGAGGTAC 1147
Db 125 AAAAAATGAACAAACAAACAACTTACTAATGAGGTAC 89
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## RESULT 12

```
US-09-328-475C-318/c
; Sequence 318, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 318
; LENGTH: 744
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```

; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(744)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-318

```

Query Match	30.0%;	Score 581;	DB 4;	Length 744;
Best Local Similarity	98.1%;	Pred. No. 1.6e-151;		
Matches 619;	Conservative 0;	Mismatches 7;	Indels 5;	Gaps 3;
QY	517	GGGGCGCATCTCGAATTTGGCTTAAAGACATCATTTTAAACATAGGCAACTTCTTAT	576	
Db	744	GGGCCGAGATTNGAATGG--TAAAGACATGCATTTTAAACATAG--CAACTCTTAT	689	
QY	577	TTCTTTTCTTTTAAAAATACATAGCATTAATCCAAATCCTATTTTAAAGACCTGACAGCT	636	
Db	688	TTCTTTCTTTTAAAAATACATAGCATTAATCCAAATCCTATTTTAAAGCCNTGACAGCT	629	
QY	637	TGACAAGGTCACACTACTGCAATTTATAGACCTTCTCGTGGTTCCTGCTTTAGTTTGAAGT	696	
Db	628	TGAGAAGGTCACACTACTGCAATTTATAGGACCTTCTCGTGGTTCCTGCTTTAGTTTGAAGT	569	
QY	697	CTGCAATCCTTTGAGAAATCTTTTGCATGACAGAGGAGTAAAGAGGTAATTTGGAATTTTCACAG	509	
Db	568	CTGCAATCCTTTGAGAAATCTTTTGCATGACAGAGGAGTAAAGAGGTAATTTGGAATTTTCACAG	756	
QY	757	GGAGAACACAGCGCGAGAATGAAGGCCGAGGCTTACTGAGGCTCTCCAGTGGAGGGCTCA	816	
Db	508	GGAGAACACAGCGCGAGAATGAAGGCCGAGGCTTACTGA-GCTGTCAGTGGAGGGCTCA	450	
QY	817	TGGGTGGGACATGGAAGAAAGGCGAGCCTTTGAGGAAAAGGCTTAAGAAAAGGAAAACCATCTCAAAA	936	
Db	449	TGGGTGGGACATGGAAGAAAGGCGAGCCTTAGGCCCTGGGAGCCAGTCCACTGACGCAAG	876	
QY	877	CAAGGACCTGAGTGAGCCTTTTGGGAAAGGCTTTGAGGAAAAGGCTTAAGAAAAGGAAAACCATCTCAAAA	330	
Db	389	CAAGGACCTGAGTGAGCCTTTTGGGAAAGGCTTTGAGGAAAAGGCTTAAGAAAAGGAAAACCATCTCAAAA	330	
QY	937	CACAAACAGAAAACCTGTCCAAATGCTTTGGGAACTGTCTTATTTGGCCTATTAATGGTCCCC	996	
Db	329	CACAAACAGAAAACCTGTCCAAATGCTTTGGGAACTGTCTTATTTGGCCTATTAATGGTCCCC	270	
QY	997	AAATGGGTAACTTACACTTCAGAGAAATGACAGAGCAAAAGGAGAAAATCTGGCTGT	1056	
Db	269	AAATGGGTAACTTACACTTCAGAGAAATGACAGAGCAAAAGGAGAAAATCTGGCTGT	210	
QY	1057	CCTTCCATTTTCAATCTGTATCTCAGGTCAGCTGGTAGGGGAGACATTAGAAAAAAA	1116	
b	209	CCTTCCATTTTCAATCTGTATCTCAGGTCAGCTGGTAGGGGAGACATTAGAAAAAAA	150	
Y	1117	TGAACACAAAACAAATTAATAGGTTAC	1147	
b	149	TGAACACAAAACAAATTAATAGGTTAC	119	

RESULT 13

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US-09-328-475C-19
/ Sequence 19, Application US/09328475C
/ Patent No. 6476207
/ GENERAL INFORMATION:
/ APPLICANT: Zhang, Jimmy
/ APPLICANT: Astel, Jon H.
/ APPLICANT: Carroll III, Eddie
/ APPLICANT: Endege, Willson O.
/ APPLICANT: Ford, Donna M.
/ APPLICANT: Monahan, John E.
/ APPLICANT: Schlegel, Robert
/ APPLICANT: Steinmann, Kathleen E.
/ TITLE OF INVENTION: GENES AND GENE EXPRESSION
/ FILE REFERENCE: ARE DIFFERENTIAL
/ FILE REFERENCE: 1532.002/200130.463

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: CURRENT APPLICATION NUMBER: US/09/328,475C
:
: CURRENT FILING DATE: 1999-06-09
:
: NUMBER OF SEQ ID NOS: 341
:
: SOFTWARE: FastSeq for Windows Version 3.0
:
: SEQ ID NO 19
:
: LENGTH: 980
:
: TYPE: DNA
:
: ORGANISM: Homo Sapien
:
: FEATURE:
:
: NAME/KEY: misc feature
:
: LOCATION: (1)..(980)
:
: OTHER INFORMATION: n = A,T,C or G
:
: US-09-328-475C-19

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Query Match	27.9%;	Score 539.6;	DB 4;	Length 980;
Best Local Similarity	92.7%;	Pred. No. 5.7e-140;		
Matches 635;	Conservative 0;	Mismatches 42;	Indels 8;	Gaps 7;
QY	448	CTTTTNTGNTTTTTTTTTTTTCGGTCTCCCAAAGCTTTATCTGCTTGACTTTTTA	507	
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QY	508	AAAAAGTTTGGGGCAGATTCTGAATTGGGTCTAAAGACATGCACTTTTTTAAACCTGGCA	567	
Db	62	AAAAAGTTTGGGGCAGATTCTGAATT-GGCTAAAGACATGCACTTTTTTAAACCTAG--C	118	
QY	568	ACTTCTTATTTCTTCTCTTAAATAATACATGACATTAATCCCAAACTCTATTTAAAGAC	627	
Db	119	AACCTCTATTTCTTCTCTTAAATAATACATGACATTAATCCCAAACTCTATTTAAAGAC	178	
QY	628	CTGACAGCTTGAGAAGGTCACTACTGCACTTTATAGGACCTTCTGGTGGTCTGCTGTAC	687	
Db	179	CTGACAGCTTGAGAAGGTCACTACTGCACTTTATAGGACCTTCTGGTGGTCTGCTGTAC	238	
QY	688	GTTTGAAGTCTGCACAACTCTTGAGAACTCTTGCAATGCGAGGAGTAAAGAGTATTCGAT	747	
Db	239	GTTTGAAGTCTGCACAACTCTTGAGAACTCTTGCAATGCGAGGAGTAAAGAGTATTCGAT	298	
QY	748	TTTTCACAGAGGAAGAACACAGCGCAGAAATGAAGGGCCAGGCTTACTGAGGCTCTCCAGTG	807	
Db	299	TTTTCACAGAGGAAGAACACAGCGCAGAAATGAAGGGCCAGGCTTACTGA-CTGTCCAGTG	357	
QY	808	GAGGGCTCATGGTGGGACATGGAAGAGGAGGAGCTAGGCCCTGGGAGGCCAGTCCA	867	
Db	358	GAGGGCTCATGGTGGGACATGGAAGAGGAGGAGCCTAGGCCCTGGGAGGCCAGTCCA	417	
QY	868	CTGAGCAAGGAGGACTGAGT-AGCCCTTTTGAGGAAAGGCTAAGAAAAGGAAAC	926	
Db	418	CTGAGCAAGGAGGAGGACTGAGTGAAGCCTTTTGAGGAAAGGCTAAGAAAAGGAAAC	477	
QY	927	CAATCTAAAAACACAAAGAACTGTCCCAATGCTTTGGAACTGTGTTTATTCGCTATA	986	
Db	478	CAATCTAAAAACACAAAGAACTGTCCCAATGCTTTGGAACTGTGTTTATTCGCTATA	537	
QY	987	ATGGGTCCCCAAAT-GGGTAACTAGACTTCAGAGAGAAATGAGCAGAGAGCAAA-GGAG	1044	
Db	538	ATGGGTCCCCAAATGGGGTAAACTAGACTTCAGAGAGAAATGAGCAGAGAGCAAA-GGAG	597	
QY	1045	AAATCTGGCTGCTCTCC-ATTTTTCATCTGTGTTATCTCAGGTGAGCTGGTAGGGGAGA	1103	
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QY	1104	CATTAGAAAAAATGAAACACAAA	1128	
Db	658	GAGANCAATTNGNANAATAATNGAAA	682	

RESULT 14  
US-09-439-313-434  
; Sequence 434, Application US/09439313  
; Patent No. 6329505  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan Louise  
APPLICANT: Jiang Yuqui  
APPLICANT: Reed, Steven G.  
APPLICANT: Kalos, Michael  
APPLICANT: Fanger, Gary  
APPLICANT: Retter, Mark  
APPLICANT: Solk, John  
APPLICANT: Day, Craig  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
FILE REFERENCE: 210121.427C9  
CURRENT APPLICATION NUMBER: US/09/439,313  
CURRENT FILING DATE: 1999-11-12  
NUMBER OF SEQ ID NOS: 575  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 434  
TYPE: DNA  
LENGTH: 484  
ORGANISM: Homo sapiens  
US-09-439-313-434

Query Match 24.2%; Score 469.4; DB 4; Length 484;  
Best Local Similarity 99.2%; Pred. No. 1.2e-120;  
Matches 483; Conservative 0; Mismatches 1; Indels 3; Gaps 1;  
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Db 1 TTTTAAATAAGCATTTAGTGGCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG 60  
QY 1473 AATTTAATCTTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATGATATTG 1532  
Db 61 AATTTAATCTTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATGATATTG 120  
QY 1533 TGTTCAGNGAAGAAAGAAAGTGTCTTTGTTTAAATTAATTTGTTTGTGATCCATCT 177  
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QY 1593 TGTCTTTTCCCAATGGAACTAGTCAATTAACCCATCTCTGAACCTGTGAGAAACATCTG 1652  
Db 178 TGTCTTTTCCCAATGGAACTAGTCAATTAACCCATCTCTGAACCTGTGAGAAACATCTG 237  
QY 1653 AAGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGTTCTCAGAACCAATTTCAACC 1712  
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QY 1833 AACTTTATTTTCTATGTTGTTTGGCAACATATGAGTGTGTTTGAATAAAGTACCCAT 1892  
Db 418 AACTTTATTTTCTATGTTGTTTGGCAACATATGAGTGTGTTTGAATAAAGTACCCAT 477  
QY 1893 GTCTTTA 1899  
Db 478 GTCTTTA 484

## RESULT 15

US-09-352-616A-434  
Sequence 434, Application US/09352616A  
Patent No. 6395278  
GENERAL INFORMATION:  
APPLICANT: Dillon, Davin C.  
APPLICANT: Harlocker, Susan Louise  
APPLICANT: Jiang, Yuqui  
APPLICANT: Xu, Jiangchun

APPLICANT: Mitcham, Jennifer Lynn  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS  
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE  
FILE REFERENCE: 210121.427C8  
CURRENT APPLICATION NUMBER: US/09/352,616A  
CURRENT FILING DATE: 1999-07-13  
NUMBER OF SEQ ID NOS: 472  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 434  
LENGTH: 484  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-352-616A-434

Query Match 24.2%; Score 469.4; DB 4; Length 484;  
Best Local Similarity 99.2%; Pred. No. 1.2e-120;  
Matches 483; Conservative 0; Mismatches 1; Indels 3; Gaps 1;  
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Db 1 TTTTAAATAAGCATTTAGTGGCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG 60  
QY 1473 AATTTAATCTTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATGATATTG 1532  
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QY 1533 TGTTCAGNGAAGAAAGAAAGTGTCTTTGTTTAAATTAATTTGTTTGTGATCCATCT 1592  
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Db 178 TGTCTTTTCCCAATGGAACTAGTCAATTAACCCATCTCTGAACCTGTGAGAAACATCTG 237  
QY 1653 AAGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGTTCTCAGAACCAATTTCAACC 1712  
Db 238 AAGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGTTCTCAGAACCAATTTCAACC 297  
QY 1713 AGACAGCCTGTTTCTATCTCTGTTTAAATTAATTTAGTTTGGGTTTCTTACATGATACACAA 1772  
Db 298 AGACAGCCTGTTTCTATCTCTGTTTAAATTAATTTAGTTTGGGTTTCTTACATGATACACAA 357  
QY 1773 CCTGCTCCAATCTGTACATATAAAGTCTGTGACTTTAGTTAGTACAGACCCCAACCA 1832  
Db 358 CCTGCTCCAATCTGTACATATAAAGTCTGTGACTTTAGTTAGTACAGACCCCAACCA 417  
QY 1833 AACTTTATTTTCTATGTTGTTTGGCAACATATGAGTGTGTTTGAATAAAGTACCCAT 1892  
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QY 1893 GTCTTTA 1899  
Db 478 GTCTTTA 484

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Sequence: 1 atgtgtatgccaaacttaagt.....gggcggccgcgactagtga 1936

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Searched: 1517243 seqs, 1124081882 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1836.4	94.9	2984	9	US-09-759-143-335
2	1836.4	94.9	2984	9	US-09-780-669-335
3	1836.4	94.9	2984	9	US-09-822-827-335
4	1836.4	94.9	2984	10	US-09-232-880-335
5	1836.4	94.9	2984	10	US-09-895-793-335
6	1836.4	94.9	2984	10	US-09-895-814-335
7	1836.4	94.9	2984	13	US-10-012-896-335
8	1836.4	94.9	2984	14	US-10-010-940-335
9	1645.6	85.0	3266	14	US-10-208-823-282
10	1388.8	71.7	2051	13	US-10-202-193-334
11	686.2	35.4	755	10	US-09-925-300-258
12	641.2	33.1	1024	13	US-10-202-193-81
13	628.4	32.5	1024	13	US-10-202-193-96
14	628.2	32.4	1024	13	US-10-202-193-82
15	622	32.1	1024	13	US-10-202-193-95
16	615.6	31.8	1013	13	US-10-202-193-14

c	17	611.8	31.6	724	10	US-09-768-827-85	Sequence 85, Appl
c	18	584.6	30.2	948	13	US-10-202-193-23	Sequence 23, Appl
c	19	582.2	30.1	720	13	US-10-202-193-319	Sequence 319, Appl
c	20	581	30.0	744	13	US-10-202-193-318	Sequence 318, Appl
c	21	580.6	30.0	716	10	US-09-768-827-68	Sequence 68, Appl
c	22	544.4	28.1	663	10	US-09-768-827-63	Sequence 63, Appl
c	23	539.6	27.9	980	13	US-10-202-193-19	Sequence 19, Appl
c	24	488	25.2	691	10	US-09-768-827-76	Sequence 76, Appl
c	25	477	24.6	697	10	US-09-768-827-77	Sequence 77, Appl
c	26	476.8	24.6	579	10	US-09-768-827-59	Sequence 59, Appl
c	27	469.4	24.2	484	9	US-09-759-143-434	Sequence 434, Appl
c	28	469.4	24.2	484	9	US-09-780-669-434	Sequence 434, Appl
c	29	469.4	24.2	484	9	US-09-822-827-434	Sequence 434, Appl
c	30	469.4	24.2	484	10	US-09-895-793-434	Sequence 434, Appl
c	31	469.4	24.2	484	10	US-09-895-814-434	Sequence 434, Appl
c	32	469.4	24.2	484	13	US-10-012-896-434	Sequence 434, Appl
c	33	469.4	24.2	484	14	US-10-010-940-434	Sequence 434, Appl
c	34	461.6	23.8	582	10	US-09-768-827-78	Sequence 78, Appl
c	35	447.4	23.1	553	10	US-09-768-827-58	Sequence 58, Appl
c	36	446.6	23.1	683	10	US-09-768-827-90	Sequence 90, Appl
c	37	426.2	22.0	731	10	US-09-768-827-55	Sequence 55, Appl
c	38	421.6	21.8	1020	13	US-10-202-193-102	Sequence 102, Appl
c	39	421.6	21.8	1021	13	US-10-202-193-103	Sequence 103, Appl
c	40	411	21.2	822	13	US-10-202-193-223	Sequence 223, Appl
c	41	378.2	19.5	497	13	US-10-202-193-222	Sequence 222, Appl
c	42	358.8	18.5	374	10	US-09-969-708-40	Sequence 40, Appl
c	43	350.4	18.1	366	9	US-09-759-143-115	Sequence 115, Appl
c	44	350.4	18.1	366	9	US-09-780-669-115	Sequence 115, Appl
c	45	350.4	18.1	366	9	US-09-030-606-115	Sequence 115, Appl

ALIGNMENTS

RESULT 1  
US-09-759-143-335  
; Sequence 335, Application US/09759143  
; Patent No. US2002002248A1  
; GENERAL INFORMATION:

- APPLICANT: Xu, Jiangchun
- APPLICANT: Dillon, Davin C.
- APPLICANT: Mitcham, Jennifer L.
- APPLICANT: Harlocker, Susan L.
- APPLICANT: Jiang, Yuqi
- APPLICANT: Henderson, Robert A.
- APPLICANT: Kalos, Michael D.
- APPLICANT: Fanger, Gary R.
- APPLICANT: Retter, Marc W.
- APPLICANT: Stolk, John H.
- APPLICANT: Day, Craig H.
- APPLICANT: Vedwick, Thomas S.
- APPLICANT: Carter, Darrick
- APPLICANT: Li, Samuel
- APPLICANT: Wang, Aijun
- APPLICANT: Skeiky, Yasir A.W.
- APPLICANT: Hepler, William
- TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
- FILE REFERENCE: 210121.427C23
- CURRENT APPLICATION NUMBER: US/09/759,143
- CURRENT FILING DATE: 2001-01-12
- NUMBER OF SEQ ID NOS: 934
- SOFTWARE: FastSeq for Windows Version 3.0
- SEQ ID NO 335
- LENGTH: 2984
- TYPE: DNA
- ORGANISM: Homo sapien

US-09-759-143-335

Query Match 94.9%; Score 1836.4; DB 9; Length 2984;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 1897; Conservative 0; Mismatches 12; Indels 7; Gaps 5;

QY	1	AATG	TATGCCAACTTAAGTATTTACAGGGTGGCCCAATAAGAACAGATGCATCGCTG	60
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QY	61	TGAT	TTTAAAGCAAGCTGTATAAACAGAACTCCACTGCAAGAGGNGGGCCGGCCAGGA	120
Db	1127	TGAT	TTTAAAGCAAGCTGTATAAACAGAACTCCACTGCAAGAGGNGGGCCGGCCAGGA	1186
QY	121	GAAT	CTCGCTTGTCCAAAGACAGGGGCTTAAGAGGGGTCTCCACATGCTGCTAGGGGCT	180
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QY	181	GTTC	CAATTTTTTATTAGTAGAAGTGAAGAGGCTCTTCTCAACTTTTTTCCCTTGGC	240
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QY	241	TGGAGA	TTTGAATCAGAACTTCCCTGGAGTTTTCCAGGCTATCATATATACGTATTCCT	300
Db	1307	TGGAGA	TTTGAATCAGAACTTCCCTGGAGTTTTCCAGGCTATCATATATACGTATTCCT	1366
QY	301	GAAGG	CAACATAATCTTCCTCCCTCCCTTTTAAATTTTGTGTTCTCTTTTGCAGCAA	360
Db	1367	GAAGG	CAACATAATCTTCCTCCCTCCCTTTTAAATTTTGTGTTCTCTTTTGCAGCAA	1426
QY	361	TTACT	CACTAAAGGGCTTCATTTTAGTCCAGATTTTTTAGTCTGGCTGCACCTAACTTATG	420
Db	1427	TTACT	CACTAAAGGGCTTCATTTTAGTCCAGATTTTTTAGTCTGGCTGCACCTAACTTATG	1486
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Db	1487	CCTCG	CTATTAGCCGAGATCTGGTCTTTTTTTT - TTTTTTTTTTTTTTCCGCTCTCC	1544
QY	481	CAAA	AGCTTTATCTCTCTTGACTTTTTTAAAAAGTTTGGGGCAGATTCTGAAATTTGGGCTA	540
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QY	661	AGG	ACTTCTGGTGTCTGCTGTTACGTTTGAAGTCTGCAATCCTTGAGAACTTTTGC	720
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Db	1842	GGCC	AGGCTTACTGAG - GCTGTCCAGTGGAGGGCTCATGGTGGGACATGCGAAAGAGGC	1900
QY	841	AGC	TAGGCCCTGGGAGCCCATCTCAGTCAGCAAGCAAGGAGCTGAGTGAGCCTTTTGC	900
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Db	2021	TTTGG	AACTGTGTTTTATTGCTTATATGGTGTCCCAAAATGGGTAACTAGACTTCAGA	2080
QY	1021	GAGA	ATGACAGAGCAAGGAGAAATCTGGCTGTCTTCCATTTTTCATCTCTGTATCT	1080
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Db	2141		CAGGTGAGCTGGTAGGGGAGACATTTAGAAAAAATGAACAAACAAAACAAATTA	2200
Qy	1141		GAGGTACGCTGAGCGCTGGGAGTCTCTTGACTCCACTACTTAATCCGTTTAGTGAGAAA	1200
Db	2201		GAGGTACGCTGAGCGCTGGGAGTCTCTTGACTCCACTACTTAATCCGTTTAGTGAGAAA	2260
Qy	1201		CCTTTCAAATTTCTTTTATTAGAAGGCCAGCTTACTGTGTGGGCAAAATTCGCAACAT	1260
Db	2261		CCTTTCAAATTTCTTTTATTAGAAGGCCAGCTTACTGTGTGGGCAAAATTCGCAACAT	2320
Qy	1261		AAGTTAATAGAAAGTGGCCAAATTCACCCCAATTTCTGTGTGGTTCGGCTCCACATTGCA	1320
Db	2321		AAGTTAATAGAAAGTGGCCAAATTCACCCCAATTTCTGTGTGGTTCGGCTCCACATTGCA	2380
Qy	1321		ATGTTCAATGCGACGTGCTGCTGACACCGACCGAGTACTAGCCAGCACAAAAGGCAGGG	1380
Db	2381		ATGTTCAATGCGACGTGCTGCTGACACCGACCGAGTACTAGCCAGCACAAAAGGCAGGG	2440
Qy	1381		TAGCCTCAATTCGTTCTGCTCTTTACATTTCTTTTAAATAAGCATTTTAGTGCTCAGTC	1440
Db	2441		TAGCCTCAATTCGTTCTGCTCTTTACATTTCTTTTAAATAAGCATTTTAGTGCTCAGTC	2500
Qy	1441		CCTACTGAGTACTCTTTCTCTCCCTCCCTGCTGAATTAATCTTTCACTGCAATTTGC	1500
Db	2501		CCTACTGAGTACTCTTTCTCTCCCTCCCTGCTGAATTAATCTTTCACTGCAATTTGC	2560
Qy	1501		AAGGATTACACATTTCACTGTGATGATATATGTGGTTGCGAGNAAAGAAAAAGTGCTT	1560
Db	2561		AAGGATTACACATTTCACTGTGATGATATATGTGGTTGCGA - AAAAAAATAAGTGCTT	2619
Qy	1561		TGTTTAAATTTACTCTGGTTTGTAATCCATCTGCTTTTCCCATTTGGAACCTAGTCAT	1620
Db	2620		TGTTTAAATTTACTCTGGTTTGTAATCCATCTGCTTTTCCCATTTGGAACCTAGTCAT	2679
Qy	1621		AACCCATCTCTGAACTGGTAGAAAAACATCTGAAGAGCTTAGTCTATCAGCATCTCACAGG	1680
Db	2680		AACCCATCTCTGAACTGGTAGAAAAACATCTGAAGAGCTTAGTCTATCAGCATCTCACAGG	2739
Qy	1681		TGAATTTGGATGGTTCTCAGAACATTTGACCCAGACAGCGCTGTTTCTATCTGTTTAAATA	1740
Db	2740		TGAATTTGGATGGTTCTCAGAACATTTGACCCAGACAGCGCTGTTTCTATCTGTTTAAATA	2799
Qy	1741		AAATTAGTTTGGGTTCTCTACATGCAATAACAAACCGCTCCAACTCTGTCACATAAAGTC	1800
Db	2800		AAATTAGTTTGGGTTCTCTACATGCAATAACAAACCGCTCCAACTCTGTCACATAAAGTC	2859
Qy	1801		TGTGACTTGAGTTTAGTCAGCACCCCCCAACCAATTTATTTTCTATGTGTTTTTGTCA	1860
Db	2860		TGTGACTTGAGTTTAGTCAGCACCCCCCAACCAATTTATTTTCTATGTGTTTTTGTCA	2919
Qy	1861		ACATATGAGTGTTTTGAAATAAAGTACCCATGCTCTTTTATTTAAANANAAAAAAA	1916
Db	2920		ACATATGAGTGTTTTGAAATAAAGTACCCATGCTCTTTTATTTAGAAAAAATAAAAA	2975

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RESULT 2
US-09-780-669-335
; Sequence 335, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitchell, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Mark W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.

```



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Db      2860 TGTGACTTGAAGTTTGTAGTCAGACCCACCCACCAACTTTATTTTCTATGCTTTTGTGCA 2919
Qy      1861 ACATATGAGCTGTTTGAATAAAGTAAGTACCACTGCTTTATTAATAAATAAATAAATAA 1916
Db      2920 ACATATGAGCTGTTTGAATAAAGTAAGTACCACTGCTTTATTAATAAATAAATAAATAA 2975

RESULT 3
US-09-822-827-335
; Sequence 335, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 2984
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-335

Query Match      94.9%; Score 1836.4; DB 9; Length 2984;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 189; Conservative 0; Mismatches 12; Indels 7; Gaps 5;

Qy      1 AATGGTATGCCAACTTAAAGTATTACAGGGTGGCCCAATAGACAGAGTCACTCGCTG 60
Db      1067 AATGGTATGCCAACTTAAAGTATTACAGGGTGGCCCAATAGACAGAGTCACTCGCTG 60
Qy      61 TGAATTTTAAAGACAGCTGTATATAAAGAGTCTTCTCACTGCAAGAGGCGGCGGCGCAGGA 1126
Db      1127 TGAATTTTAAAGACAGCTGTATATAAAGAGTCTTCTCACTGCAAGAGGCGGCGGCGCAGGA 120
Qy      121 GAATCTCGCTTGTCCAAAGAGGGGCTTAAGAGGCTTCCACACTGCTGTAGGGGCT 180
Db      1187 GAATCTCGCTTGTCCAAAGAGGGGCTTAAGAGGCTTCCACACTGCTGTAGGGGCT 1246
Qy      181 GTTGCAATTTTATTAGTAGAAGTGAAGAGGCTTCTCACTGCTGTAGGGGCT 1246
Db      1247 GTTGCAATTTTATTAGTAGAAGTGAAGAGGCTTCTCACTGCTGTAGGGGCT 240
Qy      241 TGGAGATTTAGAAATCAGAGTTCCTCGAGTTCCTAGGAGTTCCTCACTGCTGTAGGGGCT 300
Db      1307 TGGAGATTTAGAAATCAGAGTTCCTCGAGTTCCTAGGAGTTCCTCACTGCTGTAGGGGCT 1366
Qy      301 GAAAGGCAACATAATCTCTCCCTCTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 360
Db      1367 GAAAGGCAACATAATCTCTCCCTCTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 1426
Qy      361 TTACTCACTAAGGGCTTCATTTTATGTCAGATTTTATGTCGGCTGCACTTAATG 420
Db      1427 TTACTCACTAAGGGCTTCATTTTATGTCAGATTTTATGTCGGCTGCACTTAATG 420
Qy      421 CCTCGCTTATTTAGCCGAGATCTGCTCTTTTNTGNTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1486
Db      1487 CCTCGCTTATTTAGCCGAGATCTGCTCTTTTNTGNTTTTTTTTTTTTTTTTTTTTTTTTTTTT 480
Qy      481 CAAAGCTTTATCTGCTTCACTTTTAAAGAGTTCGGGCGAGATTCGTAATGGGCTA 1544
Db      1545 CAAAGCTTTATCTGCTTCACTTTTAAAGAGTTCGGGCGAGATTCGTAATGGGCTA 540
Qy      541 AAAGACATGCATTTTAAAGTACAGCACTTCTTATTTCTTTCTTTTAAATAATACATAGC 1603
Db      1604 AAAGACATGCATTTTAAAGTACAGCACTTCTTATTTCTTTCTTTTAAATAATACATAGC 600
Qy      601 ATTAAATCCCAATCCTATTTAAAGACCTGACAGCTGAGAGTCACTGCTGATTTAT 660
Db      1601 ATTAAATCCCAATCCTATTTAAAGACCTGACAGCTGAGAGTCACTGCTGATTTAT 660
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Db      1662 ATTAAATCCCAATCCTATTTAAAGACCTGACAGCTTGAGAGGTCACCTACTGCTATTTAT 1721
Qy      661 AGGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db      1722 AGGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1781
Qy      721 ATGCAGAGGAGGTAAGAGGTAATTTTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Db      1782 ATGCAGAGGAGGTAAGAGGTAATTTTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Qy      781 GGCAGGCTTACTGAGGCTGCTCAGTGGAGGCTCATGGGTGGGACATGGGAGGAGGAGGAGGAG 840
Db      1842 GGCAGGCTTACTGAGGCTGCTCAGTGGAGGCTCATGGGTGGGACATGGGAGGAGGAGGAGGAG 1900
Qy      841 AGCTAGGCTTGGGAGGCTTGGGAGGCTTGGGAGGCTTGGGAGGCTTGGGAGGCTTGGGAGGCTT 900
Db      1901 AGCTAGGCTTGGGAGGCTTGGGAGGCTTGGGAGGCTTGGGAGGCTTGGGAGGCTTGGGAGG 900
Qy      901 AGGAAAGGCTAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1960
Db      1961 AGGAAAGGCTAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
Qy      961 TTTGGGAACTGTTTATGCTTATAATGGTCTTCCCAAAATGGGTAACCTGCTGCTGCTGCTGCT 2020
Db      2021 TTTGGGAACTGTTTATGCTTATAATGGTCTTCCCAAAATGGGTAACCTGCTGCTGCTGCTGCT 2140
Qy      1081 CAGGTGAGCTGTTAGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
Db      2141 CAGGTGAGCTGTTAGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2200
Qy      1141 GAGGTACGCTGAGGCTTGGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Db      2201 GAGGTACGCTGAGGCTTGGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2260
Qy      1201 CCTTTCAATTTCTTTTATTAGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
Db      2261 CCTTTCAATTTCTTTTATTAGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2320
Qy      1261 AAGTTAATAGAAAGTGGGCAATTTTCAACCCATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
Db      2321 AAGTTAATAGAAAGTGGGCAATTTTCAACCCATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 2380
Qy      1321 ATGTTCAATGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
Db      2381 ATGTTCAATGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2440
Qy      1381 TAGCCTGAATTTCTGCTGCTTTCAGATTTTCTTTTAAATTAAGCATTTAGTGTCTGCTGCTGCT 1440
Db      2441 TAGCCTGAATTTCTGCTGCTTTCAGATTTTCTTTTAAATTAAGCATTTAGTGTCTGCTGCTGCT 2500
Qy      1441 CCTACTGAGTACTCTTCTCTCCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
Db      2501 CCTACTGAGTACTCTTCTCTCCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2560
Qy      1501 AAGGATTACACATTTTCACTGCTGATATATGTTGTCAGNGAGAAAGGAGGAGGAGGAGGAGGAG 1560
Db      2561 AAGGATTACACATTTTCACTGCTGATATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2619
Qy      1561 TGTTTAAATTTACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2679
Db      2620 TGTTTAAATTTACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1620
Qy      1621 AACCCATCTCTGAACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1680
Db      2680 AACCCATCTCTGAACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2739
Qy      1681 TGAATTTGATGTTTCTGAGAAACCATTTTCAACCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1740
Db      2740 TGAATTTGATGTTTCTGAGAAACCATTTTCAACCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2799
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QY 1741 AATTAGTTGGTCTCTCATGATTAACAAACCCCTGCTCCAATCTGTCTCATATAAAGTC 1800  
DB 2800 AATTAGTTGGTCTCTCATGATTAACAAACCCCTGCTCCAATCTGTCTCATATAAAGTC 2859  
QY 1801 TGTGACTTGAAGTTAGTACGACCCGCCACCAACTTATTTCTCTATGTGTTTTTGGCA 1860  
DB 2860 TGTGACTTGAAGTTAGTACGACCCGCCACCAACTTATTTCTCTATGTGTTTTTGGCA 2919  
QY 1861 ACATATGAGTGTGTTGAAATTAAGTACCCATGCTCTTTATTAATAAANAANAANA 1916  
DB 2920 ACATATGAGTGTGTTGAAATTAAGTACCCATGCTCTTTATAGAAAAAANAANA 2975

RESULT 4  
US-09-232-880-335  
; Sequence 335, Application US/09232880  
; Publication No. US20020182596A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer Lynn  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF  
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.428C6  
; CURRENT APPLICATION NUMBER: US/09/232,880  
; CURRENT FILING DATE: 1999-01-15  
; NUMBER OF SEQ ID NOS: 338  
; SOFTWARE: Fast-Seq for Windows Version 3.0  
; SEQ ID NO 335  
; LENGTH: 2984  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-232-880-335

Query Match 94.9%; Score 1836.4; DB 10; Length 2984;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 1897; Conservative 0; Mismatches 12; Indels 7; Gaps 5;

QY 1 AATGGTATGCAACTTAAGTATTTACAGGGTGGCCCAATAGAACAGATGCATCGCTG 60  
DB 1067 AATGGTATGCAACTTAAGTATTTACAGGGTGGCCCAATAGAACAGATGCATCGCTG 1126

QY 61 TGATTTTAAAGCAAGCTGTATAACAGAACTCCACTGCAAGAGGGGGCCGGCCAGGA 120  
DB 1127 TGATTTTAAAGCAAGCTGTATAACAGAACTCCACTGCAAGAGGGGGCCGGCCAGGA 1186

QY 121 GAATCTCCGCTTCCNAGACAGGGGCTTAAGAGGGTCTCCACACTGCTGTAGGGGCT 180  
DB 1187 GAATCTCCGCTTCCNAGACAGGGGCTTAAGAGGGTCTCCACACTGCTGTAGGGGCT 1246

QY 181 GTTGCAATTTTATTTAGTAAAGTGGAAAGGCTCTTCTCAACTTTTTCCTTTGGGC 240  
DB 1247 GTTGCAATTTTATTTAGTAAAGTGGAAAGGCTCTTCTCAACTTTTTCCTTTGGGC 1306

QY 241 TGGAGATTTAGAAATCAGAAAGTTTCTGGAGTTTTCAGGCTATCATATATCTGTATCCT 300  
DB 1307 TGGAGATTTAGAAATCAGAAAGTTTCTGGAGTTTTCAGGCTATCATATATCTGTATCCT 1366

QY 301 GAAGGCAACATAATTTCTTCTTCCCTCTTAAATTTTGTGTTCCCTTTTGGAGCAA 360  
DB 1367 GAAGGCAACATAATTTCTTCTTCCCTCTTAAATTTTGTGTTCCCTTTTGGAGCAA 1426

QY 361 TTACTCACTAAAGGGCTTCAATTTTGTCCAGATTTTGTGCTGGCTGCACCTTAACATTATG 420  
DB 1427 TTACTCACTAAAGGGCTTCAATTTTGTCCAGATTTTGTGCTGGCTGCACCTTAACATTATG 1486

QY 421 CCTCGCTTATTTAGCCCGAGATCTGCTCTTTTNTGNTTTTTTTTTTTCGCTCTCC 480  
DB 1487 CCTCGCTTATTTAGCCCGAGATCTGCTCTTTTNTGNTTTTTTTTTTTCGCTCTCC 1544

QY 481 CAAGCTTATCTGCTTGAATTTTAAAGTTTGGGGGCGAGATTCGAAATGGGGCTA 540

DB 1545 CAAAGCTTTATCTGCTTGACATTTTAAAGTTTGGGGGCGAGATTCGAAAT -GGCTA 1603  
QY 541 AAAGCATGCAATTTTAAAGTACAGCACTTCTTATTTCTTTCTTTTAAATAATACATAGC 600  
DB 1604 AAAGCATGCAATTTTAAAGTACAGCACTTCTTATTTCTTTCTTTTAAATAATACATAGC 1661  
QY 601 ATTAAATCCCAATCTCTATTAAAGACCTGACAGCTTGAGAAAGGTCACTATGCAATTTAT 660  
DB 1662 ATTAAATCCCAATCTCTATTAAAGACCTGACAGCTTGAGAAAGGTCACTATGCAATTTAT 1721  
QY 661 AGGACCTTCTGCTGGTCTGCTGTTTACGTTTGAAGTCTGACAACTCTTCCAGAAATCTTTGC 720  
DB 1722 AGGACCTTCTGCTGGTCTGCTGTTTACGTTTGAAGTCTGACAACTCTTCCAGAAATCTTTGC 1781  
QY 721 ATGCAGAGGAGTAAAGAGGTATTGGATTTTACAGAGGAAGAACACAGCGCAGAAATGAAG 780  
DB 1782 ATGCAGAGGAGTAAAGAGGTATTGGATTTTACAGAGGAAGAACACAGCGCAGAAATGAAG 1841  
QY 781 GGCCAGGCTTACTGAGGCTGTCCAGTGGAGGCTCATGAGTGGGACATCGGAAAGAGGC 840  
DB 1842 GGCCAGGCTTACTGA -GCTGTCCAGTGGAGGCTCATGAGTGGGACATCGGAAAGAGGC 1900  
QY 841 AGCCTAGGCCCTGGGGAGGCCAGTCCACTGACGACGAGGAGCTGAGTGAGCCTTTTGC 900  
DB 1901 AGCCTAGGCCCTGGGGAGGCCAGTCCACTGACGACGAGGAGCTGAGTGAGCCTTTTGC 1960  
QY 901 AGGAAAGGCTAAGAAAGAGGAAACCAATTTTAAAGACAAACAAAGAAACTGTCCAAATGC 960  
DB 1961 AGGAAAGGCTAAGAAAGAGGAAACCAATTTTAAAGACAAACAAAGAAACTGTCCAAATGC 2020  
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DB 2021 TTTGGGAATCTGTTTATTTGCTTATAATGGTCTCCCAATGGTAACTAGACTTTCAG 2080  
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DB 2141 CAGGTGAGCTGTAGAGGGGAGACATTTAGAAAAAATAAGAAAAAATAAGAACTTACTAAT 2200  
QY 1141 GAGGTACGCTGAGGCTGAGGAGTCTCTTGACTTCCACTACTTAATTCCTGTTTGTAGAAA 1200  
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DB 2261 CTTTTCAATTTTCTTTTATTAGAAGGGCAGCTTACTGTTGTCGCAAAATTTGCCAAT 2320  
QY 1261 AAGTTAATAGAAAGTTGGCCAAATTTCAACCCCAATTTCTGTTGTTGGGCTCCACATTTGCA 1320  
DB 2321 AAGTTAATAGAAAGTTGGCCAAATTTCAACCCCAATTTCTGTTGTTGGGCTCCACATTTGCA 2380  
QY 1321 ATGTTCAATGCAACGCTGCTGTGACACCGACCGGAGTACTAGCCAGCAACAAAGGCGAGG 1380  
DB 2381 ATGTTCAATGCAACGCTGCTGTGACACCGACCGGAGTACTAGCCAGCAACAAAGGCGAGG 2440  
QY 1381 TAGCCTGAATTTGCTTCTTCTTTTACATTTCTTTTAAATAAGCAATTTAGTGTCTCAGTC 1440  
DB 2441 TAGCCTGAATTTGCTTCTTCTTCTTTTACATTTCTTTTAAATAAGCAATTTAGTGTCTCAGTC 2500  
QY 1441 CCTACTGAGTACTCTTCTCTCCCTCTCTCAATTTTAAATTTCTTCACTTGTCAATTTTGC 1500  
DB 2501 CCTACTGAGTACTCTTCTCTCCCTCTCTCTGANTTTAATTTCTTCACTTGTCAATTTTGC 2560  
QY 1501 AAGGATTAACATTTCTACTGTGATGATATATTGTGTGAGNGAAAGAAAAAGTGTCTT 1560  
DB 2561 AAGGATTAACATTTCTACTGTGATGATATATTGTGTGAGNGAAAGAAAAAGTGTCTT 2619  
QY 1561 TGTTTTAAATTTACTTGGTGTGTGGAATCCATCTTGTCTTTTCCCAATTTGGAATAGTCAAT 1620  
DB 2620 TGTTTTAAATTTACTTGGTGTGTGGAATCCATCTTGTCTTTTCCCAATTTGGAATAGTCAAT 2679

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QY 1621 AACCATCTCTGAAGTCTAGAAACATCTGAAGAGCTAGTCTATCAGCATCTCAGAGG 1680
Db |||||
QY 2680 AACCATCTCTGAAGTCTAGAAACATCTGAAGAGCTAGTCTATCAGCATCTCAGAGG 2739
Db |||||
QY 1681 TGAATTGATGTTCTCAGAACCATTTACCCAGAGCAGCTCTGTTCTATCTGTTTAATA 1740
Db |||||
QY 2740 TGAATTGATGTTCTCAGAACCATTTACCCAGAGCAGCTCTGTTCTATCTGTTTAATA 2799
Db |||||
QY 1741 AATTAGTTTGGGTTCTCTACATGATCAATAACAAACCTGCTCCAACTGTGCATATAAAGTC 1800
Db |||||
QY 2800 AATTAGTTTGGGTTCTCTACATGATCAATAACAAACCTGCTCCAACTGTGCATATAAAGTC 2859
Db |||||
QY 1801 TGTGACTTGAAGTTTGTAGTCAGCACCCCAACCAACTTTTATTTTCTATGTTTGTGCA 1860
Db |||||
QY 2860 TGTGACTTGAAGTTTGTAGTCAGCACCCCAACCAACTTTTATTTTCTATGTTTGTGCA 2919
Db |||||
QY 1861 ACATATGAGTGTGTTTGAATAAAGTACCCATGCTTTTATTAATAAATAAATAAATAA 1916
Db |||||
QY 2920 ACATATGAGTGTGTTTGAATAAAGTACCCATGCTTTTATTAATAAATAAATAAATAA 2975
Db |||||

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## RESULT 5

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US-09-895-793-335
; Sequence 335, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitchem, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; CURRENT REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 2984
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-793-335

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Query Match 94.9%; Score 1836.4; DB 10; Length 2984;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1897; Conservative 0; Mismatches 12; Indels 7; Gaps 5;

QY 1 AATGGTATGCCAATTAAGTATTTACAGGGTGGCCCAATAGAAAGATGCACTCGCTG 60
Db |||||
QY 1067 AATGGTATGCCAATTAAGTATTTACAGGGTGGCCCAATAGAAAGATGCACTCGCTG 1126
Db |||||
QY 61 TGATTTTACAGCAAGCTGTATTAACAGAACTCCACTGCAAGAGGCGGCGGCCAGGA 120
Db |||||
QY 1127 TGATTTTACAGCAAGCTGTATTAACAGAACTCCACTGCAAGAGGCGGCGGCCAGGA 1186
Db |||||

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QY 121 GAATCTCGCTTGTCCCAAGACAGGGGCTAAGAGGGGTCTCCACACTGTGCTAGGGGCT 180
Db |||||
QY 1187 GAATCTCGCTTGTCCCAAGACAGGGGCTAAGAGGGGTCTCCACACTGTGCTAGGGGCT 1246
Db |||||
QY 181 GTTGCAATTTTATTAAGTAGAAGTGGAAGGCGCTCTTCTCAACTTTTCCCTTGGGC 240
Db |||||
QY 1247 GTTGCAATTTTATTAAGTAGAAGTGGAAGGCGCTCTTCTCAACTTTTCCCTTGGGC 1306
Db |||||
QY 241 TGGAGAAATTTAGAAATCAGAGTTTCTGAGTTTTCAGGCTATCATATATATCTGATCT 300
Db |||||
QY 1307 TGGAGAAATTTAGAAATCAGAGTTTCTGAGTTTTCAGGCTATCATATATATCTGATCT 1366
Db |||||
QY 301 GAAAGGCAACATTAATTTCTCTTCCCTCTTAAATTTTAAATTTTAAATTTTAAATTTTAA 360
Db |||||
QY 1367 GAAAGGCAACATTAATTTCTCTTCCCTCTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1426
Db |||||
QY 361 TTACTCACTAAAGGGCTTCAATTTTAGTCAGATTTTAAATTTTAAATTTTAAATTTTAAATTT 420
Db |||||
QY 1427 TTACTCACTAAAGGGCTTCAATTTTAGTCAGATTTTAAATTTTAAATTTTAAATTTTAAATTT 1486
Db |||||
QY 421 CTGCGCTTATTTAGCCCGAGATCTGGTCTTTTNTGTTTNTGTTTNTGTTTNTGTTTNTGTTTNT 480
Db |||||
QY 1487 CTGCGCTTATTTAGCCCGAGATCTGGTCTTTTNTGTTTNTGTTTNTGTTTNTGTTTNTGTTTNT 1544
Db |||||
QY 481 CAAAGCTTTATCTGCTTGTGACTTTTAAAGTTTGGGGGCGAGATTTCTGAATTTGGGCTA 540
Db |||||
QY 1545 CAAAGCTTTATCTGCTTGTGACTTTTAAAGTTTGGGGGCGAGATTTCTGAATTTGGGCTA 1603
Db |||||
QY 541 AAAGACATGCAATTTTAAACTAGGCAACTCTTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 600
Db |||||
QY 1604 AAAGACATGCAATTTTAAACTAGGCAACTCTTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1661
Db |||||
QY 601 ATTAATCCCAATCTTATTTAAAGCTGAGCTGAGAGGTCACACTGCTGCTGCTGCTGCTGCTGCT 720
Db |||||
QY 1662 ATTAATCCCAATCTTATTTAAAGCTGAGCTGAGAGGTCACACTGCTGCTGCTGCTGCTGCTGCT 1721
Db |||||
QY 661 AGGACCTTCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db |||||
QY 1722 AGGACCTTCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1781
Db |||||
QY 721 ATGACAGAGGAGTAAAGAGGTATTGGAATTTTACAGAGGAAGAACACAGCGCAGAGTGAAG 1841
Db |||||
QY 1782 ATGACAGAGGAGTAAAGAGGTATTGGAATTTTACAGAGGAAGAACACAGCGCAGAGTGAAG 1841
Db |||||
QY 781 GGCACGGCTTACTGAGGCTGTCCAGTGGAGGCTCATGCGTGGGAGGCTCATGCGTGGGAGGCTCATG 840
Db |||||
QY 1842 GGCACGGCTTACTGAGGCTGTCCAGTGGAGGCTCATGCGTGGGAGGCTCATGCGTGGGAGGCTCATG 1900
Db |||||
QY 841 AGCTAGGCGCTTGGGAGGCGCCAGTCCACTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 900
Db |||||
QY 1901 AGCTAGGCGCTTGGGAGGCGCCAGTCCACTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1960
Db |||||
QY 901 AGGAAAGGCTAAGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAA 960
Db |||||
QY 1961 AGGAAAGGCTAAGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAA 2020
Db |||||
QY 961 TTTGGGAACTGCTGTTTATTTGCTTATTAATGGGTCCCAAAATGGGTAACTGAGTCTGAGCCTTTTGC 1020
Db |||||
QY 2021 TTTGGGAACTGCTGTTTATTTGCTTATTAATGGGTCCCAAAATGGGTAACTGAGTCTGAGCCTTTTGC 2080
Db |||||
QY 1021 GAGATGAGCAGAGCAAGAGGAGAAATCTGGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1080
Db |||||
QY 2081 GAGATGAGCAGAGCAAGAGGAGAAATCTGGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2140
Db |||||
QY 1081 CAGTGTAGCTGTGAGGGGAGACATTAGAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1140
Db |||||
QY 2141 CAGTGTAGCTGTGAGGGGAGACATTAGAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2200
Db |||||
QY 1141 GAGTGTAGCTGTGAGGGGAGACATTAGAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1200
Db |||||
QY 2201 GAGTGTAGCTGTGAGGGGAGACATTAGAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2260
Db |||||

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1201 CCTTCAATTTCTTTTATAGAGGCGCCAGCTTACTGTGTGGCAAAATGCCAACAT 1260  
Db CCTTCAATTTCTTTTATAGAGGCGCCAGCTTACTGTGTGGCAAAATGCCAACAT 2320  
1261 AGGTAATAGAAAGTTGGCAATTTCCACCCCATTTCTGTGGTTGGGCTCCACATTGCA 1320  
Db AGGTAATAGAAAGTTGGCAATTTCCACCCCATTTCTGTGGTTGGGCTCCACATTGCA 2380  
1321 ATGTTCAATGCCAGTGTCTGCTGACACCGAGTACTAGCCAGCAGCAAAAGGCGAGG 1380  
Db ATGTTCAATGCCAGTGTCTGCTGACACCGAGTACTAGCCAGCAGCAAAAGGCGAGG 2440  
1381 TAGCCTGAATGTCTTCTGCTCTTTACATTTCTTTAAATAAGCAATTTAGTGTCTCAGTC 1440  
Db TAGCCTGAATGTCTTCTGCTCTTTACATTTCTTTAAATAAGCAATTTAGTGTCTCAGTC 2500  
1441 CCTACTGAGTACTCTTCTCTCCCTCTCTGAAATTTAAATCTTTTCAACTTGAATTTGC 1500  
Db CCTACTGAGTACTCTTCTCTCCCTCTCTGAAATTTAAATCTTTTCAACTTGAATTTGC 2560  
1501 AAGGATTACACATTTCACTGTGATATATTTGTTGTCAGNAGAAAGAAAGTGTCTT 1560  
Db AAGGATTACACATTTCACTGTGATATATTTGTTGTCAGNAGAAAGAAAGTGTCTT 2619  
1561 TGTAAAATTAATCTGGTTTGAATCCATCTTGTCTTTTCCCATTTGAACTAGTCAAT 1620  
Db TGTAAAATTAATCTGGTTTGAATCCATCTTGTCTTTTCCCATTTGAACTAGTCAAT 2679  
1621 ACCCATCTCTGAACTGTAGAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGG 1680  
Db ACCCATCTCTGAACTGTAGAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGG 2739  
1681 TGAATTTGATGGTTCTCAGAACCATTTACCCAGACAGCGCTGTTCTATCTCTGTTTAAATA 1740  
Db TGAATTTGATGGTTCTCAGAACCATTTACCCAGACAGCGCTGTTCTATCTCTGTTTAAATA 2799  
1741 AATTAGTTGGGTTCTCTACATGCAATAAACCCTGCTCCAATCTGTCAATAAAAGTC 1800  
Db AATTAGTTGGGTTCTCTACATGCAATAAACCCTGCTCCAATCTGTCAATAAAAGTC 2859  
1801 TGTGACTTGAAGTTTGTAGTACGACACCCCAACCACTTTATTTCTATGTGTTTTTGCA 1860  
Db TGTGACTTGAAGTTTGTAGTACGACACCCCAACCACTTTATTTCTATGTGTTTTTGCA 2919  
1861 ACATATGAGTGTGTTTGAATAAAGTACCCATGCTCTTTATTAATAAATAAATAAATA 1916  
Db ACATATGAGTGTGTTTGAATAAAGTACCCATGCTCTTTATTAATAAATAAATAAATA 2975

RESULT 6  
US-09-895-814-335  
; Sequence 335, Application US/09895814  
; Publication No. US20020193296A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Horal, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.

; APPLICANT: Vinals de Bassols, Carlota  
; APPLICANT: Foy, Teresa  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.427C26  
; CURRENT APPLICATION NUMBER: US/09/895,814  
; SOFTWARE: FastSeq for Windows Version 3.0  
; NUMBER OF SEQ ID NOS: 990  
; SEQ ID NO 335  
; LENGTH: 2984  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-895-814-335  
Query Match 94.9%; Score 1836.4; DB 10; Length 2984;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 1897; Conservative 0; Mismatches 12; Indels 7; Gaps 5;  
1 AATGGTATGCCAACTTAAGTATTTACAGGGTGGCCCAATAGAACAAAGATGCATCGCTG 60  
Db 1067 AATGGTATGCCAACTTAAGTATTTACAGGGTGGCCCAATAGAACAAAGATGCATCGCTG 1126  
61 TGAATTTAAGACAAGCTGTATAAACAAGAACTCCACTGCAAGAGGNGGCCGGGCCAGGA 120  
Db 1127 TGAATTTAAGACAAGCTGTATAAACAAGAACTCCACTGCAAGAGGNGGCCGGGCCAGGA 1186  
121 GAATCTCCGCTTGTCCAAGACAGGGGCTTAAGAGGGTCTCCACACTGCTGTAGGGCT 180  
Db 1187 GAATCTCCGCTTGTCCAAGACAGGGGCTTAAGAGGGTCTCCACACTGCTGTAGGGCT 1246  
181 GTTGCATTTTATTTATTTAGTAGAAAGTGGAAAGGCTCTTCTCAACTTTTTCCTTTGGGC 240  
Db 1247 GTTGCATTTTATTTATTTAGTAGAAAGTGGAAAGGCTCTTCTCAACTTTTTCCTTTGGGC 1306  
241 TGGAGAAATTTAGAATCAGAAGTTTCTGGAGTTTTCAGGCTATCATATATATCTATCT 300  
Db 1307 TGGAGAAATTTAGAATCAGAAGTTTCTGGAGTTTTCAGGCTATCATATATATCTATCT 1366  
301 GAAAGGCAACATAATCTTCTCCCTCTTTTAAATTTTGTGTTCTTTTTCAGCA 360  
Db 1367 GAAAGGCAACATAATCTTCTCCCTCTTTTAAATTTTGTGTTCTTTTTCAGCA 1426  
361 TTACTCCTAAAGGGCTTCATTTTATAGTCCAGATTTTATAGTCTGGCTGCACCTTAATG 420  
Db 1427 TTACTCCTAAAGGGCTTCATTTTATAGTCCAGATTTTATAGTCTGGCTGCACCTTAATG 1486  
421 CCTCGCTTATTTAGCCCGAGATCTGGTCTTTTNTGNTTTTNTTTTNTTTCCTCTCC 480  
Db 1487 CCTCGCTTATTTAGCCCGAGATCTGGTCTTTTNTT - TTTTNTTTCCTCTCC 1544  
481 CAAAGCTTTATCTGTCTTGACTTTTAAAGAGTTTGGGGCAGATTCTGAATTTGGCTA 540  
Db 1545 CAAAGCTTTATCTGTCTTGACTTTTAAAGAGTTTGGGGCAGATTCTGAATTTGGCTA 1603  
541 AAAGACATGCATTTTAAAGAACTAGCACTTCTTATTTCTTTTAAATAATACATAGC 600  
Db 1604 AAAGACATGCATTTTAAAGAACTAGCACTTCTTATTTCTTTTAAATAATACATAGC 1661  
601 ATTAATCCCAATCCTATTTAAAGACCTGACAGCTTGAGAAAGTCACTACTGCAATTTAT 660  
Db 1662 ATTAATCCCAATCCTATTTAAAGACCTGACAGCTTGAGAAAGTCACTACTGCAATTTAT 1721  
661 AGGACCTTCTGGTGTCTGCTGTTTGAAGTCTGACATCTCTTGAGAAATCTTTGC 720  
Db 1722 AGGACCTTCTGGTGTCTGCTGTTTGAAGTCTGACATCTCTTGAGAAATCTTTGC 1781  
721 ATGACAGAGGTAAGAGTATTTGATTTTCAAGAGGAAGAACACAGCGCAAGATGAAG 780  
Db 1782 ATGACAGAGGTAAGAGTATTTGATTTTCAAGAGGAAGAACACAGCGCAAGATGAAG 1841  
781 GGCCAGGGCTTACTGAGGCTGTCCAGTGGAGGGCTCATGGTGGGACATCGGAAAGAGGC 840

Db 1842 GGCACAGGCTTACTGA-GCTGTCAGTGGAGGCTCTAGGGTGGGACATGAAAGAGGC 1900  
QY 841 AGCCTAGGCTTGGGAGCCCGAGTCCACTGAGCAAGCAAGGACTGAGTGGCTTTTGC 900  
Db 1901 AGCCTAGGCTTGGGAGCCCGAGTCCACTGAGCAAGCAAGGACTGAGTGGCTTTTGC 1960  
QY 901 AGGAAAGGCTTAAGAAAGGAAAGCAACCATCTTAAACACACACAGAACTGTCTCAATGC 960  
Db 1961 AGGAAAGGCTTAAGAAAGGAAAGCAACCATCTTAAACACACACAGAACTGTCTCAATGC 2020  
QY 961 TTTGGGAAGCTGTTTATGCTTAAATGGGTCCCAAAATGGGTAACTAGACTTTCAGA 1020  
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QY 1021 GAGAAATGAGCAGAGAGCAAGAGGAGAAATCTGGCTGTCTTCAATTTTCACTGTATCT 1080  
Db 2081 GAGAAATGAGCAGAGAGCAAGAGGAGAAATCTGGCTGTCTTCAATTTTCACTGTATCT 2140  
QY 1081 CAGGTGAGCTGTTAGAGGGGAGACATTTAGAAAGAAATGAAACAAACAAACAACTACTAT 1140  
Db 2141 CAGGTGAGCTGTTAGAGGGGAGACATTTAGAAAGAAATGAAACAAACAACTACTAT 2200  
QY 1141 GAGTACGCTGAGGCTGGGAGTCTCTGACTCCACTACTTAATTCGGTTAGTGAGAAA 1200  
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QY 1201 CCTTCAATTTCTTTTATGAGAGGCGCAGCTTACTGTGGTGCAAAATGGCCACAT 1260  
Db 2261 CCTTCAATTTCTTTTATGAGAGGCGCAGCTTACTGTGGTGCAAAATGGCCACAT 2320  
QY 1261 AAGTTAATAGAAAGTTGGCCAAATTTACCCCAATTTCTGGTTGGGCTCCACATTTGCA 1320  
Db 2321 AAGTTAATAGAAAGTTGGCCAAATTTACCCCAATTTCTGGTTGGGCTCCACATTTGCA 2380  
QY 1321 ATGTTCAATGCAAGTGTCTGTGACACGACCGAGTACTAGCCAGACAAAGGAGGG 1380  
Db 2381 ATGTTCAATGCAAGTGTCTGTGACACGACCGAGTACTAGCCAGACAAAGGAGGG 2440  
QY 1381 TAGCCTGAATTCCTTCTGCTCTTTTACATTTCTTTTAAATAGCAATTTAGTCTCAGTC 1440  
Db 2441 TAGCCTGAATTCCTTCTGCTCTTTTACATTTCTTTTAAATAGCAATTTAGTCTCAGTC 2500  
QY 1441 CTTACTAGTACTCTTCTCTCCCTCTCTGAAATTTAAATTTCTTTTAAATAGCAATTTAGTCTCAGTC 2560  
Db 2501 CTTACTAGTACTCTTCTCTCCCTCTCTGAAATTTAAATTTCTTTTAAATAGCAATTTAGTCTCAGTC 2560  
QY 1501 AAGGATACATTTCTGCTGATGATATATGTTGACGAGGAAAGAAAGTGTCTT 1560  
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Db 2620 TGTTTAAATTAATGTTGTTGTAATCCATCTTCTTTTCCCAATTTGCA-AAAAAAGTGTCTT 1620  
QY 1621 AACCCTCTGAGCTGTTAGAAACATCTGAAGAGTGTATCTATCAGCATCTGACAGG 1680  
Db 2680 AACCCTCTGAGCTGTTAGAAACATCTGAAGAGTGTATCTATCAGCATCTGACAGG 2739  
QY 1681 TGAATGGATGGTCTCAGAACCAATTTTCCACGAGCAGCTGTTTCTATCTCTGTTTAAATA 1740  
Db 2740 TGAATGGATGGTCTCAGAACCAATTTTCCACGAGCAGCTGTTTCTATCTCTGTTTAAATA 2799  
QY 1741 AATTAGTTGGTCTCTACATGATCAFAACAAACCTGTCTTCAATCTGTACATAAAGTC 1800  
Db 2800 AATTAGTTGGTCTCTACATGATCAFAACAAACCTGTCTTCAATCTGTACATAAAGTC 2859  
QY 1801 TGTGACTTGAAGTTAGTCAGACACCCCAACAACTTTTATTTTCTATGTTTGTGCA 1860  
Db 2860 TGTGACTTGAAGTTAGTCAGACACCCCAACAACTTTTATTTTCTATGTTTGTGCA 2919  
QY 1861 ACATATGAGTGTGTTGAAATTAAGTACCCATGCTTTTATTTAAAGGAAAAA 1916  
Db 1916 ACATATGAGTGTGTTGAAATTAAGTACCCATGCTTTTATTTAAAGGAAAAA 1916

Db 2920 ACATATGAGTGTGTTGAAATTAAGTACCCATGCTTTTATTTAGAAAAA 2975  
RESULT 7  
US-10-012-896-335  
; Sequence 335, Application US/10012896  
; Publication No. US20020183251A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darriek  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Vinals de Bassols, Carlota  
; APPLICANT: Foy, Teresa  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Wantanabe, Yoshihiro  
; APPLICANT: Megher, Madeleine Joy  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.427C27  
; CURRENT APPLICATION NUMBER: US/10/012,896  
; CURRENT FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 1011  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 335  
; LENGTH: 2984  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-012-896-335

Query Match 94.9%; Score 1836.4; DB 13; Length 2984;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 1897; Conservative 0; Mismatches 12; Indels 7; Gaps 5;  
QY 1 AATGGTATGCCAACTTAAAGTATTACAGGGTGGCCCAATAGAACAGATGCACTCGCTG 60  
Db 1067 AATGGTATGCCAACTTAAAGTATTACAGGGTGGCCCAATAGAACAGATGCACTCGCTG 1126  
QY 61 TGAATTTTAAAGCAAGCTGTATATAACAGAACTCCACTGCAAGAGGGGGGGCCGAGCA 120  
Db 1127 TGAATTTTAAAGCAAGCTGTATATAACAGAACTCCACTGCAAGAGGGGGGGCCGAGCA 1186  
QY 121 GAATCTCCCTTGTCTCAAGACAGGGCCCTAGGAGGGTCTCCACACTGCTGTAGGGCT 180  
Db 1187 GAATCTCCCTTGTCTCAAGACAGGGCCCTAGGAGGGTCTCCACACTGCTGTAGGGCT 1246  
QY 181 GTTGCAATTTTATTTAGTGAAGAGGGCTCTTCTCAACTTTTTCCTTCCCTTGGG 240  
Db 1247 GTTGCAATTTTATTTAGTGAAGAGGGCTCTTCTCAACTTTTTCCTTCCCTTGGG 1306  
QY 241 TGGAGAAATTTAGATCAGAACTTTTCTGGAGTTTTCAGGCTATCATATATATCTATCT 300  
Db 1307 TGGAGAAATTTAGATCAGAACTTTTCTGGAGTTTTCAGGCTATCATATATATCTATCT 1366  
QY 301 GAAAGGCAACATAATCTTCTCCCTCTTTTAAATTTTGTGTTCTTTTTCGACAA 360  
Db 1367 GAAAGGCAACATAATCTTCTCCCTCTTTTAAATTTTGTGTTCTTTTTCGACAA 1426





	PRIOR FILING DATE: 2001-08-22	
	PRIOR APPLICATION NUMBER: 60/325,020	
	PRIOR FILING DATE: 2001-09-25	
	PRIOR APPLICATION NUMBER: 60/341,746	
	PRIOR FILING DATE: 2001-12-12	
	PRIOR APPLICATION NUMBER: 60/362,158	
	PRIOR FILING DATE: 2002-03-05	
	NUMBER OF SEQ ID NOS: 455	
	SOFTWARE: FastSeq for Windows Version 4.0	
	SEQ ID NO 282	
	LENGTH: 3266	
	TYPE: DNA	
	ORGANISM: Homo sapiens	
	US-10-205-823-282	
	Query Match 85.0%; Score 1645.6; DB 14; Length 3266;	
	Best Local Similarity 95.8%; Pred. No. 0;	
	Matches 1826; Conservative 0; Mismatches 47; Indels 34; Gaps 12;	
Qy	1 AATGGTATGCCAACTTAAGTATTACAGGTGCGCCAAATAGAACAAAGATGCACTCGCTG 60	
Db	1373 AATGGTATGCCAACTTAAGTATTACAGGTGCGCCAAATAGAACAAAGATGCACTCGCTG 1432	
Qy	61 TGATTTTAAGACACAGCTGTATAACAGNACTCCA CTGCAAGAGGNGGGCGGGCCAGGA 120	
Db	1433 TGATTTTAAGACAAGCTGTATAAACAAGACTCCA CTGCAAGAGGAGGGCGGGCCAGGA 1492	
Qy	121 GAATCTCCGCTGTGCCAAGCAGGGGCTTAAGGAGGGTCTCCACACTGCTGCTAGGGGCT 180	
Db	1493 GAATCTCCGCTGTGCCAAGCAGGGGCTTAAGGAGGGTCTCCACACTGCTGCTAGGGGCT 1552	
Qy	181 GTTGCAITTTTTTATTATAGTAGAAAGTGGAAAGGCCTCTTCTCAACTTTTTTCCCCTGGGC 240	
Db	1553 GTTGCAITTTTTTATTATAGTAGAAAGTGGAAAGGCCTCTTCTCAACTTTTTTCCCCTGGGC 1612	
Qy	241 TGGAGAATTTAGAATCAGAAGTTTCTCGAGTTTTCAGGCTATCATATATACGTATCCT 300	
Db	1613 TGGAGAATTTAGAATCAGAAGTTTCTCGAGTTTTCAGGCTATCATATATACGTATCCT 1672	
Qy	301 GAAAGGCCAACATAATCTCTCCCTCCCTTTTAAAAATTTTGTCTTCCCTTTTGCAGCAA 360	
Db	1673 GAAAGGCCAACATAATCTCTCCCTCCCTTTTAAAAATTTTGTCTTCCCTTTTGCAGCAA 1732	
Qy	361 TTACTCACTAAAGGGCTTCATTTTAGTCCAGATTTT TAGTCTGGCTGCACCTAACTTATG 420	
Db	1733 TTACTCACTAAAGGGCTTCATTTTAGTCCAGATTTT TAGTCTGGCTGCACCTAACTTATG 1792	
Qy	421 CCTCGCTATTATAGCCGAGATCTGGTCTTTTNTN TGTNTTTTTTTTTTCCGCTCCC 480	
Db	1793 CCTCGCTATTATTAGCCGAGATCCGGTCTTTTT - - - - -TTTTTTTTTTTTTTCCGCTCCC 1848	
Qy	481 CAAAGCTTTATCTGCTTGACTTTTTTAAAAAGTTTGGGGGCGAGTTCTGAAITTTGGGCTA 540	
Db	1849 CAAAGCTTTATCTGCTTGACTTTTTTAAAAAGTTTGGGGGCGAGTTCTGAAITTTGGGCTA 1907	
Qy	541 AAAGACATGCATTTTTTAAAAC TAGGCAACTTCTTATTTCTTTCTTAAAAATACATAGC 600	
Db	1908 AAAGACATGCATTTTTTAAAAC TAG - CAAC TCTTATTTCTTTCTTTAAAAATACATAGC 1965	
Qy	601 ATTAATCCCAATCCTATTTTAAAGACCTGACAGCTTGAGAA - GGTCAC TACTGCATTTA 659	
Db	1966 ATTAATCCCAATCCTATTTTAAAGACCTGACAGCTTGAGAAAGGGTCACTACTGCAATTTA 2025	
Qy	660 TAGGACCTCTGGTGGTTCTGCTGTTAGCTTTGAGCTTGAGTCTGCAATCCTTGAGATCTTTG 719	
Db	2026 TAGGACCTCTGGTGGTTCTGCTGTTAGCTTTGAGCTTGAGTCTGCAATCCTTGAGATCTTTG 2085	
Qy	720 CATGCAGAGGAGGTAAAGGCTATTGGATTTTCA GAG - GGAAGAACACAGCGCAGAAATGA 778	
Db	2086 CATGCAGAGGAGGTAAAGGCTATTGGATTTTCA GAGAGGAGAGNACACAGCGCAGAAATGA 2145	
Qy	779 AGGCCACAGGCTTACTGAGGCTGTCCAGTGGAGGGCTCATCGGTGGGACATGGGAAAGAAG 838	

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RESULT 10
US-10-202-193-334/c
; Sequence 334, Application US/10202193
; Publication No. US20020192699A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; CURRENT APPLICATION NUMBER: US/10/202,193
; CURRENT FILING DATE: 2002-07-23
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 334
; LENGTH: 2051
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2051)
; OTHER INFORMATION: n = A,T,C or G
US-10-202-193-334.

Query Match          71.7%; Score 1398.8; DB 13; Length 2051;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1438; Conservative 1; Mismatches 12; Indels 5; Gaps 4;

Qy      449  TTATTTTNGTNTTTTTTTTTTTCGGTCTCCCAAGAGCTTATCTGTCTGCACCTTTTAA 508
Db      1814  TGTTTTTTTTTTTTTTTTTTTTTTCGGTCTCCCAAGAGCTTATCTGTCTGCACCTTTTAA 1755

Qy      509  AAAAGTTTGGGGCAGATTCTGAATTTGGGCTAAAGACATCGCANTTTTAAACTAGCAA 568
Db      1754  AAAAGTTTGGGGCAGATTCTGAATTTGGGCTAAAGACATCGCANTTTTAAAWACTAG--CA 1698

Qy      569  CTCTTATTTCCTTCTTTAAATACATAGCATTTAATCCCAATCCTATTTAAAGACC 628
Db      1697  ACTCTTATTTCCTTCTTTAAATACATAGCATTTAATCCCAATCCTATTTAAAGACC 1638

Qy      629  TCACAGCTTGAGAGGTCACCTACTGCATTTATAGGACCTTCTGTGTGTTCTGCTGTACG 688
Db      1637  TCACAGCTTGAGAGGTCACCTACTGCATTTATAGGACCTTCTGTGTGTTCTGCTGTACG 1578

Qy      689  TTTGAAGTCTGACAATCCTTCAGAAATCTTTGCGATCGAGAGAGGTAAAGAGTATTGGATT 748
Db      1577  TTTGAAGTCTGACAATCCTTCAGAAATCTTTGCGATCGAGAGAGGTAAAGAGTATTGGATT 1518

Qy      749  TTCACAGGGAAGACACAGCGCAGAAATGAAGGCCAGGCTTACTGAGGCTGTCCAGTCG 808
Db      1517  TTCACAGGGAAGACACAGCGCAGAAATGAAGGCCAGGCTTACTGAGGCTGTCCAGTCG 808

Qy      809  AGGGCTCATGGTGGGACATGGAAGAGAGGAGCGAGCTTGGAGCCAGGCTTACTGAG--CTGTCCAGTGG 1459
Db      1458  AGGGCTCATGGTGGGACATGGAAGAGAGGAGCGAGCTTGGAGCCAGGCTTACTGAG--CTGTCCAGTGG 868

Qy      869  TGACGACGAAGGACCTGAGTGGACCTTTTGAGGAAAAGGCTTAAGAAAAAGGAAACCA 928
Db      1398  TGAGCAAGCAAGGACCTGAGTGGACCTTTTGAGGAAAAGGCTTAAGAAAAAGGAAACCA 1339

Qy      929  TTCTAAACACACAGAAJACTGTCCAAATGCTTTTGGGAACTGTGTGTTTATTGCCCTAAT 988
Db      1338  TTCTAAACACACAGAAJACTGTCCAAATGCTTTTGGGAACTGTGTGTTTATTGCCCTAAT 1279

Qy      989  GGGTCCCCAAAATGGGTAACTTAGACTTCACAGAGAAATGACACAGAGCAAGAGAAAT 1048

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; CURRENT APPLICATION NUMBER: US/09/925,300  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05988  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1890  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 258  
; LENGTH: 755  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (755)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-300-258

Query Match 35.4%; Score 686.2; DB 10; Length 755;  
Best Local Similarity 98.9%; Pred. No. 2.1e-176;  
Matches 700; Conservative 1; Mismatches 5; Indels 2; Gaps 1;  
QY 1209 TTTTCTTTTATTAGAGGGCCAGCTTACTGTTGGTGCAAAATTCGCAACATAAGTTAAT 1268  
Db |||||  
38 TTTTCTTTTATTAGAGGGCCAGCTTACTGTTGGTGCAAAATTCGCAACATAAGTTAAT 97  
QY 1269 AGAAGTGTGCAATTCACCCCAATTTCTGTGTTGGGCTCCACATTCGAATGTTCAA 1328  
Db |||||  
98 AGAAGTGTGCAATTCACCCCAATTTCTGTGTTGGGCTCCACATTCGAATGTTCAA 157  
QY 1329 TGCCAGTGTGCTGACACCGGAGGAGTACTAGCCAGCAGCAGCAAAAGGCGAGGTAGCTGA 1388  
Db |||||  
158 TGCCAGTGTGCTGACACCGGAGGAGTACTAGCCAGCAGCAGCAAAAGGCGAGGTAGCTGA 217  
QY 1389 ATTGCTTTCTGCTCTTACATTTCTTTTAAATTAAGCATTTAGTGTCTCAGTCCCTACTGA 1448  
Db |||||  
218 ATTGCTTTCTGCTCTTACATTTCTTTTAAATTAAGCATTTAGTGTCTCAGTCCCTACTGA 277  
QY 1449 GTACTCTTCTCTCCCTCTCTGAAATTTAAATTTCAACTTGCATTTGCAAGGATTA 1508  
Db |||||  
278 GTACTCTTCTCTCCCTCTCTGAAATTTAAATTTCAACTTGCATTTGCAAGGATTA 337  
QY 1509 CACATTTCTGATGTATATTTGTTGTCAGNAGAAAGAAAGTGCTTTGTTTAA 1568  
Db |||||  
338 CACATTTCTGATGTATATTTGTTGTCGA--AAAAAAGAAAGTGCTTTGTTTAA 395  
QY 1569 ATTACTTGTGTTGTAATCCATCTGCTTTTCCCAATTTGGAACTAGTCAATTAACCCATC 1628  
Db |||||  
396 ATTACTTGTGTTGTAATCCATCTGCTTTTCCCAATTTGGAACTAGTCAATTAACCCATC 455  
QY 1629 TCTGAATCTGTGAGAAACATCTGAAAGAGCTAGTCTATCAGCATCTGACAGGTGAATTGG 1688  
Db |||||  
456 TCTGAATCTGTGAGAAACATCTGAAAGAGCTAGTCTATCAGCATCTGACAGGTGAATTGG 515  
QY 1689 ATGGTTCTCAGAACCAATTTACCCAGACAGCTGTTTCTATCTGTTTAAATTAATAGTT 1748  
Db |||||  
516 ATGGTTCTCAGAACCAATTTACCCAGACAGCTGTTTCTATCTGTTTAAATTAATAGTT 575  
QY 1749 TGGGTTCTCTACATGATACAAACCTGCTCCAATCTGTACATTAAGTCTGTGACTT 1808  
Db |||||  
576 TGGGTTCTCTACATGATACAAACCTGCTCCAATCTGTACATTAAGTCTGTGACTT 635  
QY 1809 GAAGTTTGTAGTCAGCACCCCAACAACTTTATTTTCTATGTTGTTTTTGCACATATGA 1868  
Db |||||  
636 GAAGTTTGTAGTCAGCACCCCAACAACTTTATTTTCTATGTTGTTTTTGCACATATGA 695  
QY 1869 GTGTTTGAATAAAGTACCCATGCTTTATTTAAATAAATAAATAA 1916  
Db |||||  
696 GTGTTTGAATAAAGTACCCATGCTTTATTTAGAAAAAATAAATAA 743

RESULT 12  
US-10-202-193-81/c

; Sequence 81, Application US/10202193  
; Publication No. US20020192699A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Jimmy  
; APPLICANT: Astell, Jon H.  
; APPLICANT: Carroll III, Eddie  
; APPLICANT: Endege, Wilson O.  
; APPLICANT: Ford, Donna M.  
; APPLICANT: Monahan, John E.  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Steinmann, Kathleen E.  
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT  
; FILE REFERENCE: PP-01532.103/200130.463D1  
; CURRENT APPLICATION NUMBER: US/10/202,193  
; CURRENT FILING DATE: 2002-07-23  
; NUMBER OF SEQ ID NOS: 341  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 81  
; LENGTH: 1024  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(1024)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-202-193-81  
Query Match 33.1%; Score 641.2; DB 13; Length 1024;  
Best Local Similarity 97.3%; Pred. No. 4.7e-164;  
Matches 681; Conservative 0; Mismatches 16; Indels 3; Gaps 3;  
QY 448 CTTTTTNTGNTTTTTTTTTTTTTTCCGTCCTCCCAAGCTTTTATCTGTCTGACATTTTAA 507  
Db 799 CTCCTTNNNNNNTTTTTTTTTTCNGTCTCCCAAGCTTTTATCTGTCTGACATTTTAA 740  
QY 508 AAAAAAGTTGGGGGAGATTCGAAATTTGGGTAAAGAGCATGCATTTTAAAGCATAGGCA 567  
Db 739 AAAAAAGTTGGGGGAGATTCGAAATTTGGGTAAAGAGCATGCATTTTAAAGCAT-GCA 682  
QY 568 ACTTCTTATTTCTTTCCTTTTAAATATACATAGCATTAATCCCAATCCATTTTAAAGAC 627  
Db 681 ACTTCTTATTTCTTTCCTTTTAAATATACATAGCATTAATCCCAATCCATTTTAAAGAC 622  
QY 628 CTGACAGCTTGAGAAAGGTCATCTACTGCAATTTATAGGACCTTCTGGTGGTTCCTGTTTAC 687  
Db 621 CTGACAGCTTGAGAAAGGTCATCTACTGCAATTTATAGGACCTTCTGGTGGTTCCTGTTTAC 562  
QY 688 GTTTGAAGTCTGACAAATCTTTGAGAAATCTTTGATGCAAGAGGATTAAGAGATTTGGAT 747  
Db 561 GTTTGAAGTCTGACAAATCTTTGAGAAATCTTTGATGCAAGAGGATTAAGAGATTTGGAT 502  
QY 748 TTTTCACAGGAGGAGCAACACAGCGCAGAAATGAGGGCCAGGCTTACTGAGGCTGTCAGTG 807  
Db 501 TTTTCACAGGAGGAGCAACACAGCGCAGAAATGAGGGCCAGGCTTACTGAGGCTGTCAGTG 443  
QY 808 GAGGCTCATGCTGGGACATGGAAGAGAGGACAGCTAGGCCCTGGGGAGGCCAGTCCA 867  
Db 442 GAGGCTCATGCTGGGACATGGAAGAGAGGACAGCTAGGCCCTGGGGAGGCCAGTCCA 383  
QY 868 CTGAGCAAGGAGGAGCTGAGTGAGCCTTTTTCAGGAGAAAGGCTAAGAAAAAGGAAAAAC 927  
Db 382 CTGAGCAAGGAGGAGCTGAGTGAGCCTTTTTCAGGAGAAAGGCTAAGAAAAAGGAAAAAC 323  
QY 928 ATTCTTAAACACAAACAGAACTGTCCAAATGCTTTGGAACTGTGTTTATTTGCTATAA 987  
Db 322 ATTCTTAAACACAAACAGAACTGTCCAAATGCTTTGGAACTGTGTTTATTTGCTATAA 263  
QY 988 TGGGTCCCCCAAAATGCGGTAACTTAGACTTTAGAGAGATGAGCAGAGCAAGAGAGAAA 1047  
Db 262 TGGGTCCCCCAAAATGCGGTAACTTAGACTTTAGAGAGATGAGCAGAGCAAGAGAGAAA 203  
QY 1048 TCTGGCTGTCTTCCATTTTTCATTTCTCTAGGTGAGCTGTTAGAGGGGAGACATT 1107



Db 202 TCTGCTGCTCTCCATTTTCATTTCTAGTGTAGTGTAGGGGAGACATT 143  
Qy 1108 AGAAAAAATGAACAACACAAACAAATTAATAGGTAC 1147  
Db 142 AGAAAAAATGAACAACAAACAAATTAATAGGTAC 103

## RESULT 13

US-10-202-193-96/c  
; Sequence 96, Application US/10202193  
; Publication No. US20020192699A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Jimmy  
; APPLICANT: Astei, Jon H.  
; APPLICANT: Carroll III, Eddie  
; APPLICANT: Endege, Wilson O.  
; APPLICANT: Ford, Donna M.  
; APPLICANT: Monahan, John E.  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Steinmann, Kathleen E.  
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT  
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER  
; FILE REFERENCE: PP-01532.103/200130.463D1  
; CURRENT APPLICATION NUMBER: US/10/202,193  
; NUMBER OF SEQ ID NOS: 341  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 96  
; LENGTH: 1024  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(1024)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-202-193-96

Query Match 32.5%; Score 628.4; DB 13; Length 1024;  
Best Local Similarity 97.4%; Pred. No. 1.5e-160;  
Matches 678; Conservative 0; Mismatches 13; Indels 5; Gaps 4;

Qy 453 TTTGTTNTTTTTTTTTTTCCTCCCAAGCTTTATCTGT-CTTGACTTTTAAAAA 511  
Db 795 TTTTNNNNTTTTTTTTTTCNGTCTCCCAAGCTTTATCGGCTTGACTTTTAAAAA 736  
Qy 512 AGTTGGGGGAGATTCTGTAATTCGGCTTAAAGACATGCATTTTAAACTAGGCACTT 571  
Db 735 AGTTGGGGGAGATTCTGTAATTCGGCTTAAAGACATGCATTTTAAACTAGGCACTT 571  
Qy 572 CTTATTTCTTTTAAAAAATACATAGCATTAATCCCAATCCCTATTAAAGACCTGA 631  
Db 678 CTTATTTCTTTTAAAAAATACATAGCATTAATCCCAATCCCTATTAAAGACCTGA 619  
Qy 632 CAGCTTGAGAGGTCACCTACTGCAATTTATAGGACCTTCTGGTGGTCTCTGTAGTTT 691  
Db 618 CAGCTTGAGAGGTCACCTACTGCAATTTATAGGACCTTCTGGTGGTCTCTGTAGTTT 559  
Qy 692 GAAGCTGCAATCTTTGAGAACTTTTGCATGCAGAGGAGGTAAGAGGTATGGAATTTTC 751  
Db 558 GAAGCTGCAATCTTTGAGAACTTTTGCATGCAGAGGAGGTAAGAGGTATGGAATTTTC 499  
Qy 752 ACAGAGAGAACACACAGCGCAGAAATGAAGGCCAGGCTTACTGAGCTGTCCAGTGGAGG 811  
Db 498 ACAGAGAGAACACACAGCGCAGAAATGAAGGCCAGGCTTACTGAGCTGTCCAGTGGAGG 440  
Qy 812 GCTCATGGGTGGACATGGAAGAGAGGAGGAGGCTAGGCCCTGGGAGGCCAGTCCACTGA 871  
Db 439 GCTCATGGGTGGACATGGAAGAGAGGAGGAGGCTAGGCCCTGGGAGGCCAGTCCACTGA 380  
Qy 872 GCAGAGAGGAGTGTAGTGTAGCTTTTTCAGGAAAGGCTTAAGAAAAAGGAAACCAATTC 931  
Db 379 GCAGAGAGGAGTGTAGTGTAGCTTTTTCAGGAAAGGCTTAAGAAAAAGGAAACCAATTC 320

Qy 932 TAAACAACAACAGAACTCTCCAAATGCTTTGGAACTGTGTTTATTCCTATAATGGG 991  
Db 319 TAAAAACAACAAGAACTGTCCAAATGCTTTGGAACTGTGTTTATTCCTATAATGGG 260  
Qy 992 TCCCCAAAATGGGTAACTTAGACTTTCAGAGAGAAATGAGCAGAGCAAAAGGAGAAATCTG 1051  
Db 259 TCCCCAAAATGGGTAACTTAGACTTTCAGAGAGAAATGAGCAGAGCAAAAGGAGAAATCTG 200  
Qy 1052 GCTGTCTCTCCATTTTCATTTCTGTTATCTCAGGTAGCTGGTAGAGGGGAGACATTAGAA 1111  
Db 199 GCTGTCTCTCCATTTTCATTTCTGTTATCTCAGGTAGCTGGTAGAGGGGAGACATTAGAA 140  
Qy 1112 AAAAATGAACAACAACAACAATTAATGAGGTAC 1147  
Db 139 AAAAATGAACAACAACAACAATTAATGAGGTAC 104

## RESULT 14

US-10-202-193-82  
; Sequence 82, Application US/10202193  
; Publication No. US20020192699A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Jimmy  
; APPLICANT: Astei, Jon H.  
; APPLICANT: Carroll III, Eddie  
; APPLICANT: Endege, Wilson O.  
; APPLICANT: Ford, Donna M.  
; APPLICANT: Monahan, John E.  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Steinmann, Kathleen E.  
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT  
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER  
; FILE REFERENCE: PP-01532.103/200130.463D1  
; CURRENT APPLICATION NUMBER: US/10/202,193  
; NUMBER OF SEQ ID NOS: 341  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 82  
; LENGTH: 1024  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(1024)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-202-193-82

Query Match 32.4%; Score 628.2; DB 13; Length 1024;  
Best Local Similarity 94.9%; Pred. No. 1.6e-160;  
Matches 690; Conservative 0; Mismatches 32; Indels 5; Gaps 4;

Qy 422 CTGCTTTATTTAGCCGAGATCTGGTCTTTTNTGCTTTTTTTTTTTTTCCTCTCCCC 481  
Db 75 CGCCTTAGCTGTGCGCGCGAGGTACTCTTTTTTTTTTTTTTTTTTTTTCCTCTCCCC 134  
Qy 482 AAGCTTTATCTCTCTGTGACTTTTAAAAAAGTTTGGGGCAGATTCTGAAATGGGCTAA 541  
Db 135 AAGCTTTATCTCTCTGTGACTTTTAAAAAAGTTTGGGGCAGATTCTGAAATGGGCTAA 193  
Qy 542 AAGCATGATTTTAAAACTAGGCACTTCTTTTCTTTTCTTTTAAAAATACATAGCA 601  
Db 194 AAGCATGATTTTAAAACTAGGCACTTCTTTTCTTTTCTTTTAAAAATACATAGCA 251  
Qy 602 TTAATCCCAATCCCTATTAAAGACCTGACAGCTTTGAGAGGTCACCTACTGCAATTATA 661  
Db 252 TTAATCCCAATCCCTATTAAAGACCTGACAGCTTTGAGAGGTCACCTACTGCAATTATA 311  
Qy 662 GGACCTTCTGGTGGTCTGCTGTTACGTTTGAAGTCTCAATCTTGAATCTTTTGA 721  
Db 312 GGACCTTCTGGTGGTCTGCTGTTACGTTTGAAGTCTCAATCTTGAATCTTTTGA 371  
Qy 722 TCAGAGGAGGTAAAGAGGTATTTGATTTTTCACAGAGGAAGAACACAGCGCAGATGAAGG 781

Db	372	TCAGAGGAGGTAAAGGGTATTGGATTTTTCAGAGGAAGAACACAGCGCAGAAATGAAGG	431
Qy	782	GCACAGGCTTACTGAGGGCTGTCCAGTGAGGGCTCATGGTGGGACATGGAAGAAAGAGGCA	841
Db	432	GCACAGGCTTACTGA-GCTGTCCAGTGAGGGCTCATGGTGGGACATGGAAGAAAGAGGCA	490
Qy	842	GCCTAGGCCCTGGGGAGCCCACTGAGCAAGCAAGGACTGAGTGAGCCCTTTTGCA	901
Db	491	GCCTAGGCCCTGGGGAGCCCACTGAGCAAGCAAGGACTGAGTGAGCCCTTTTGCA	550
Qy	902	GGAAAAAGCTAAGAAAAAGGAAACCAATCTTAAACACACAAAGAAACTGTGCCAAATGCT	961
Db	551	GGAAAAAGCTAAGAAAAAGGAAACCAATCTTAAACACACAAAGAAACTGTGCCAAATGCT	610
Qy	962	TTGGGAACCTGTGTTTATTGGCTTAATGGGTGCCCAAAATGGGTAAACCTAGACTTTCAGAG	1021
Db	611	TTGGGAACCTGTGTTTATTGGCTTAATGGGTGCCCAAAATGGGTAAACCTAGACTTTCAGAG	670
Qy	1022	AGAAATGACAGAGACAAAGAGAAATCTGGCTGTCCCTTCATTTTCATTTCTGTATCTC	1081
Db	671	AGAAATGACAGAGACAAAGAGAAATCTGGCTGTCCCTTCATTTTCATTTCTGTATCTC	730
Qy	1082	AGGTGAGCTGGTAGAGGGGAGACATTAGAAAAAAATGAAACAA-CAAAACAATTACTAAT	1140
Db	731	AGGTGAGCTGGTAAAGAGGGAGACATTGAAAAAAATGAAACAAACCAAAACCATTTACTAAT	790
Qy	1141	GAGGTAC 1147	
Db	791	GAGGTAC 797	

RESULT 15

```

US-10-202-193-95
; Sequence 95, Application US/10202193
; Publication No. US20020192699A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H. Eddie
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: PP-01532.103/200130.463D1
; CURRENT APPLICATION NUMBER: US/10/202,193
; CURRENT FILING DATE: 2002-07-23
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 95
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc:feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-10-202-193-95

```

	Query Match	32.1%	Score 622;	DB 13;	Length 1024;
	Best Local Similarity	95.0%;	Pred. No. 8.1e-159;		
	Matches 690;	Conservative 0;	Mismatches 30;	Indels 6;	Gaps 5;
Qy	453	TTTNGTNNTTTTTTTTTTCCGTCCTCCCAAGCTTTATCTGCTCTGACCTTTTAAAAAA	512		
Db	101	TTTTTTTTTTTTTTTTTTCCGTCCTCCCAAGCTTTATCTGCTCTGACCTTTTAAAAAA	160		
Qy	513	GTTTGGGGGCGAGATTCTGAATTTGGCTAAAGACATGCATTTTTTAAAACTAGGCACTTC	572		
Db	161	GTTTGGGGGCGAGATTCTGAATT--GGCTAAAGACATGCATTTTTTAAAACTAG--CAACTC	217		

Qy	573	TTATTTCTTTCC	TTAAAAATACATAGCA	TTAAATCCCAAA	TCCTATTTAAAGAC	CTGAC	632	
Db	218	TTATTTCTTTCT	TTAAAAATACATAGCA	TTAAATCCCAAA	TCCTATTTAAAGAC	CTGAC	277	
Qy	633	AGCTTGAGAAGG	TCACTACTGCAT	TTATAGGAC	CTTCTGCTGGT	CTCTGCTGTTACGTTTG	692	
Db	278	AGCTTGAGAAGG	TCACTACTGCAT	TTATAGGAC	CTTCTGCTGGT	CTCTGCTGTTACGTTTG	337	
Qy	693	AAGTCTGACAA	TCTTTTGAGAA	TCTTTGCATG	CAGAGAGG	TAAAGAGGTA	TTGATTTTCA	752
Db	338	AAGTCTGACAA	TCTTTTGAGAA	TCTTTGCATG	CAGAGAGG	TAAAGAGGTA	TTGATTTTCA	397
Qy	753	CAGAGGAAGAA	CACAGCGCAGA	ATGAAGGCC	CAGGCTTACTG	AGGCTGTCTC	AGTGGAGGG	812
Db	398	CAGAGGNAGAA	CACAGCGCAGA	TGAAGGCC	CAGGCTTACTGA	-GCTGTCC	AGTGGAGGG	456
Qy	813	CTCATGGTGGG	ACATGGAAAA	AGAGCGAC	CTTAGGCC	CTTGGGGAG	CCCACTGCAG	872
Db	457	CTCATGGTGGG	ACATGGAAAA	AGAGCGAC	CTTAGGCC	CTTGGGGAG	CCCACTGCAG	516
Qy	873	CAAGCAAGGAC	TGAGTGAGC	CTTTTTCAGG	AAAAAGCTAAG	AAAAAAG	AAAAACCA	932
Db	517	CAAGCAAGGAC	TGAGTGAGC	CTTTTTCAGG	AAAAAGGCTAAG	AAAAAAG	AAAAACCA	576
Qy	933	AAAAACAACA	CAAGAAACT	GTGTC	CAAATGCTTTGG	GAACCTGTGTT	TTATGCTATA	992
Db	577	AAAAACAACA	CAAGAAACT	GTGTC	CAAATGCTTTGG	GAACCTGTGTT	TTATGCTATA	636
Qy	993	CCCCAAAATGG	GTAACTAGAC	ACTTCAGAG	AGATGACAG	AGAGCAAG	AGAGNAATCTCG	1052
Db	637	CCCCAAAATGG	GTAACTAGAC	ACTTCAGAG	AGATGACAG	AGAGCAAG	AGAGNAATCTCG	696
Qy	1053	CTGTCTCTTCA	CTTTTTCAT	CTGTTATCT	CAGGTGAC	TCTGCTAG	AGGGGAGACAT	1112
Db	697	CTG-CC	TTCCATTTT	TCATCTCTG	NTATCTCAG	GTGAACTG	GTANANGGAGAC	1171
Qy	1113	AAAAATGAA	CAAA-CAAA	CAATTTACT	TAATGAG	TACGCTG	AGGCCTGG	1171
Db	756	AAAAATGAA	CNCAAA	CAATTTACT	TAATGAG	TACGCTG	AGGCCTGG	815
Qy	1172	TCCACT	1177					
Db	816	GCGAAT	821					

Search completed: August 26, 2003, 20:43:56  
Job time : 581 secs

Search completed: August 26, 2003, 20:43:56  
Job time : 581 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 26, 2003, 13:36:36 ; Search time 4917 Seconds  
(without alignments)

9569.548 Million cell updates/sec

Title: US-09-700-700-1

Perfect score: 1936

Sequence: 1 atgtgtatccaaactaagt.....ggggcgccgcgactagtga 1936

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.\*

1: em\_estba.\*

2: em\_esthum.\*

3: em\_estin.\*

4: em\_estnu.\*

5: em\_estov.\*

6: em\_estpl.\*

7: em\_estro.\*

8: em\_htc.\*

9: gb\_est1.\*

10: gb\_est2.\*

11: gb\_htc.\*

12: gb\_est3.\*

13: gb\_est4.\*

14: gb\_est5.\*

15: em\_estfun.\*

16: em\_estom.\*

17: em\_gss\_hum.\*

18: em\_gss\_inv.\*

19: em\_gss\_pin.\*

20: em\_gss\_vrt.\*

21: em\_gss\_fun.\*

22: em\_gss\_mam.\*

23: em\_gss\_mus.\*

24: em\_gss\_pro.\*

25: em\_gss\_rod.\*

26: em\_gss\_pbg.\*

27: em\_gss\_vrl.\*

28: gb\_gss1.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	728.4	37.6	742	13	BX102941
2	693.8	35.8	813	14	CB853124
3	689.6	35.6	851	13	BU601144
4	687.6	35.5	700	13	BU622196

C	5	643.2	33.2	674	12	BM983868
C	6	617	31.9	661	12	BQ020946
C	7	600	31.0	678	10	AW86523
C	8	599.2	31.0	608	13	BU619261
C	9	585.8	30.3	631	14	CA430903
C	10	582.2	30.1	599	9	AA813266
C	11	581.4	30.0	663	12	BQ018482
C	12	554.2	28.6	681	10	BE973555
C	13	550	28.4	563	9	AI989273
C	14	532	27.5	565	10	BF679599
C	15	521.8	27.0	538	9	AI620178
C	16	506.4	26.2	543	9	AA528104
C	17	492	25.4	504	9	AA531255
C	18	484.2	25.0	490	9	AA437224
C	19	482.2	24.9	1470	13	BQ230696
C	20	477	24.6	987	10	BF965018
C	21	448	23.1	496	9	AA516531
C	22	445	23.0	456	9	AA442287
C	23	443	22.9	472	9	AA640241
C	24	438.8	22.7	455	9	AA972883
C	25	436	22.5	488	10	BE772782
C	26	419.4	21.7	434	9	AI989281
C	27	416.8	21.5	435	9	AA809587
C	28	416	21.5	416	9	AA707108
C	29	414	21.4	414	9	AI139031
C	30	413.4	21.4	415	9	AI052805
C	31	413.4	21.4	418	9	AI791607
C	32	409	21.1	409	9	AI571633
C	33	407.4	21.0	423	9	AI685682
C	34	405.2	20.9	630	9	AI557413
C	35	404.2	20.9	445	10	BF855203
C	36	394.8	20.4	419	9	AA229495
C	37	389.2	20.1	607	12	BI855676
C	38	386	19.9	411	9	AA640928
C	39	385.4	19.9	660	9	AI525269
C	40	384.2	19.8	423	9	AA531606
C	41	380.8	19.7	403	9	AA493522
C	42	379	19.6	445	9	AA533772
C	43	375.2	19.4	431	10	BF855210
C	44	374.6	19.3	409	10	BF855199
C	45	368.8	19.0	386	9	AI027196

ALIGNMENTS

RESULT 1	BX102941	742 bp	linear	EST 06-FEB-2003
LOCUS	BX102941	Soares testis NHT Homo sapiens	cdna clone	IMAGp998M201862
DEFINITION	BX102941	IMAGE:757435, mRNA sequence.		
ACCESSION	BX102941			
VERSION	BX102941.1	GI:27845463		
KEYWORDS	EST:			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	1 (bases 1 to 742)			
AUTHORS	Ebert, L., Helli, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.			
TITLE	Human Unigeneset - RZPD3			
JOURNAL	Unpublished			
COMMENT	Contact: Ina Rolfs			
	RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH			
	Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany			
	RZPD; IMAGp998M201862.			
	RZPDLIB; I.M.A.G.E. CDNA Clone Collection;			
	Human Unigeneset - RZPD3 (RZPDLIB No.972)			
	http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972			
	Contact: Ina Rolfs			
	RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH			
	Heubnerweg 6, D-14059 Berlin, Germany			



Db	724	AAAAGAGCAGCNATAGCCCT- GGAGCCCCAGTCCACTGAGCAAGCAGNGACTGAGTGA	666
Qy	892	GCCTTTTGCAGGAAAAGGCTAAGAAAAAGGAAAAACCATTTCTAAACACACAAACAAAACTG	951
Db	665	GCCTTNTGCAGGAAAAGGCTAAGAAAAAGGAAAAACCATTTCTAAACACACAAACAAAACTG	606
Qy	952	TCCAAATGCTTTGGGAACTGTTTATTTGCTCTATAATGGGTGCCCAAAAATGGGTAACTGA	1011
Db	605	TCCAAATGCTNTGGGAACTGTTTATTTGCTCTATAATGGGTGCCCAAAAATGGGTAACTGA	546
Qy	1012	GACTTTCAGAGAGATGAGCAGAGAGAAAAGGAGAAAACTGGCTCTCTCCATTTTCATT	1071
Db	545	GACTTTCAGAGAGATGAGCAGAGAGAAAAGGAGAAAACTGGCTCTCTCCATTTTCATT	486
Qy	1072	CTGTTATCTTCAGGTGAGCTGGTAGAGGGGAGACATTAGAAAAAATGAAACAAACAAAA	1131
Db	485	CTGTTATCTTCAGGTGAGCTGGTAGAGGGGAGACATTAGAAAAAATGAAACAAACAAAA	426
Qy	1132	ATTACTAATGAGGTACGCTGAGGCGCTGGAGTCTCTTGAATCTCACTTAATTCGGTTT	1191
Db	425	ATTACTAATGAGGTACGCTGAGGCGCTGGAGTCTCTTGAATCTCACTTAATTCGGTTT	366
Qy	1192	AGTCAGAAAACTTTCAATTTTCTTTTATTAGAGGGCCAGCTTACTCTGGTGGCAAAAT	1251
Db	365	AGTCAGAAAACTTTCAATTTTCTTTTATTAGAGGGCCAGCTTACTCTGGTGGCAAAAT	306
Qy	1252	TGCCAACATTAAGTTAATAGAAAGTTGGCCAAATTTTCAACCCCAATTTCTGTGGTTGGGCTC	1311
Db	305	TGCCAACATTAAGTTAATAGAAAGTTGGCCAAATTTTCAACCCCAATTTCTGTGGTTGGGCTC	246
Qy	1312	CACATTTGCAATTTCAATATGCAACGTGTGCTGTGACACCGACGGAGTACTAGCCAGCAAA	1371
Db	245	CACATTTGCAATTTCAATATGCAACGTGTGCTGTGACACCGACGGAGTACTAGCCAGCAAA	186
Qy	1372	AAGCAGGGTAGCCCTGAATTCGCTTCTTACATTTCTTTTAAAAATAGCATTTAG	1431
Db	185	AAGCAGGGTAGCCCTGAATTCGCTTCTTACATTTCTTTTAAAAATAGCATTTAG	126
Qy	1432	TGCTCAGTCCCTACTGAGTACTCTTCTCTCCCTCTCTGAAATTTAATTTCTTTCAACTT	1491
Db	125	TGCTCAGTCCCTACTGAGTACTCTTCTCTCCCTCTCTGAAATTTAATTTCTTTCAACTT	66
Qy	1492	GCAATTTGCAAGGATTACATTTTCACTGTGATGTATATTGTGTGAGNGAAAAAGAAA	1551
Db	65	GCAATTTGCAAGGATTACATTTTCACTGTGATGTATATTGTGTGAGNGAAAAAGAAA	6
Qy	1552	AA 1553	
Db	5	AA 4	
RESULT 3			
BU601144			
LOCUS	851 bp	linear	EST 20-SEP-2002
DEFINITION	AGENCOURT 10031392 NIH MGC 142 Homo sapiens cDNA clone		
ACCESSION	IMAGE:6495018 5', mRNA sequence.		
VERSION	BU601144		
KEYWORDS	BU601144.1 GI:23252903		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
JOURNAL	1 (bases 1 to 851)		
COMMENT	NTH-MGC <a href="http://mgi.nci.nih.gov/">http://mgi.nci.nih.gov/</a> . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished Contact: Robert Straube, Ph.D. Email: <a href="mailto:cgabs@mail.nih.gov">cgabs@mail.nih.gov</a> Tissue Procurement: NCI cDNA Library Preparation: Michael Brownstein Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		

DNA Sequencing by: Amersham Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLCM2672 row: c column: 19  
 High quality sequence spot: 481.  
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   /db\_xref="taxon:9606"  
   /clone="IMAGE:6495018"  
   /tissue\_type="mixed (pool of 40 RNAs)"  
   /lab\_host="DH10B (T1-phage-resistant)"  
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   /notes="Vector: pDNR-LfB; Site 1: Sfil (ggccattatggcc);  
   Site 2: Sfil (ggccgcttcggcc). Double-stranded cDNA was  
   prepared from a pool of 40 cell line polyA+ RNAs (bladder  
   4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,  
   kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%,  
   ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary  
   gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were  
   used in cloning as follows:  
   5' - AAGCTAGAGTATCAAGCAGAGTGGCCATTACGGCGGG-3' and  
   5' - ATTCTAGAGCGCGGCGGCCACATG-AT(30)NN-3'. Full-length  
   enriched library was constructed using the Clontech  
   Creator SMART kit and size-selected to contain the >0.5 kb  
   size fraction (other fractions present in NIH MGC 141).  
   Library created in the laboratory of M. Brownstein (NIH,  
   NIH). Note: this is a NIH MGC Library. 3 others  
   254 a 174 g 236 t

BASE COUNT	254 a	174 c	184 g	236 t	3 others
ORIGIN	minim. NOTE: this is a minim. library.				
Query Match	35.6%	Score 689.6;	DB 13;	Length 851;	
Best Local Similarity	94.8%;	Pred. No. 2.8e-100;			
Matches 744;	Conservative 0;	Mismatches 37;	Indels 4;	Gaps 3;	
Qy	828	TGGAAAAGAGGCGACCTAGGCGCTGGGGAGCCGAGTCCACTGAGCAGGCAAGCAAGGACTGA	887		
Db	3	TGGAAAAGAGGCGACCTAGGCGCTGGGGAGCCGAGTCCACTGAGCAGGCAAGGAGTGA	62		
Qy	888	GTGAGCCCTTTGAGGAAAAGGCTAAGAAAAGGAAAAACCATTCTTAAAAACAACAAGAA	947		
Db	63	GTGAGCCCTTTGAGGAAAAGGCTAAGAAAAGGAAAAACCATTCTTAAAAACAACAAGAA	122		
Qy	948	ACTGTCGAATGCTTTGGGAACTGTGTTTATTTGCTTATATATGGGTCCCAAAATGGGTAA	1007		
Db	123	ACTGTCGAATGCTTTGGGAACTGTGTTTATTTGCTTATATATGGGTCCCAAAATGGGTAA	182		
Qy	1008	CCTAGACTTCAGAGAGAATCAGCAGAGAGCAAAAGGAGAAAACTCTGGCTGTCTCTTCCATTTT	1067		
Db	183	CCTAGACTTCAGAGAGAATCAGCAGAGAGCAAAAGGAGAAAACTCTGGCTGTCTCTTCCATTTT	242		
Qy	1068	CATTCTGTTATCTCAGGTGAGCTGGTAGAGGGGAGACATTAGAAAAAAAATGAAAAACAACAA	1127		
Db	243	CATTCTGTTATCTCAGGTGAGCTGGTAGAGGGGAGACATTAGAAAAAAAATGAAAAACAACAA	302		
Qy	1128	AACAATTTACTTAATGAGGTACGCTGAGSCCTGGGAGTCTCTTTGACTCCACACTACTTAATTC	1187		
Db	303	AACAATTTACTTAATGAGGTACGCTGAGSCCTGGGAGTCTCTTTGACTCCACACTACTTAATTC	362		
Qy	1188	GTTTAGTGAAAAACCTTTTCAATTTTCTTTTATTAGAGGGCCAGCTTACTTGTTGGTGCCA	1247		
Db	363	GTTTAGTGAAAAACCTTTTCAATTTTCTTTTATTAGAGGGCCAGCTTACTTGTTGGTGCCA	422		
Qy	1248	AAATTGCCACATAAGTTTAATAGAAAGTTGGCCAAATTTACCCCAATTTCTGTGTTTGG	1307		
Db	423	AAATTGCCACATAAGTTTAATAGAAAGTTGGCCAAATTTACCCCAATTTCTGTGTTTGG	482		
Qy	1308	GCTCCACATTGCAATGTTTCAATGCCAGTCTGCTGCAACCGACCGAGTACTAGCCAGC	1367		
Db	483	GCTCCACATTGCAATGTTTCAATGCCAGTCTGCTGCAACCGACCGAGTACTAGCCAGC	542		

Qy	1368	ACAAAAGCGGGTAGCCTGAATTCGTTCTGCTCTTTTACATTTCTTTTAAAAATAAGCAT	1427
Db	543	ACAAAAGCGGGTAGCCTGAATTCGTTCTGCTCTTTTACATTT - TCTTTAAATAAGCAT	601
Qy	1428	TTAGTGCTCAGTCCCTACTCAGTACTCTTTCTCTCCCTCCTCTGAAATTAATTCCTTCA	1487
Db	602	TTAGTGCTCAGTCCCTACTCAGTACTCTTTCTCTCCCTCCTCTGAAATTAATTCCTTTC	661
Qy	1488	ACTTGCAAATTCGAAGGATTACAAATTCACT - GTGATGTATATATGTTGTCAGNGAAAA	1546
Db	662	ACTTGCAAATTCGAAGGATACCAATTTTCACTGGGATGTATATGGGTTGCAAAAAAA	721
Qy	1547	GAAAAAGTCTCTTTGTTTAAATTAATCTGGTTTG - AATCACTCTGCTTTTTCCTCC	1604
Db	722	AAAAAGGGCTTTGTTTAAAAATACCTGGGNTGGGAAATCCCTCCTGCTTTTTCCTCC	781
Qy	1605	ATTGG	1609
Db	782	CATTG	786

RESULT 4	BU622196/c	700 bp	mrna	linear	EST 23-SEP-2002
LOCUS	BU622196/1				
DEFINITION	UI-H-FH1-bfu-m-08-0-UI.s1 NCI CGAP_FH1 Homo sapiens cDNA clone				
	UI-H-FH1-bfu-m-08-0-UI 3', mRNA sequence.				
ACCESSION	BU622196				
VERSION	BU622196.1	GI:23288411			
KEYWORDS	EST.				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens (human)				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 700)				
TITLE	NCI-CGAP Project ( <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .				
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),				
	Tumor Gene Index				
JOURNAL	Unpublished				
COMMENT	Contact: Robert Strausberg, Ph.D.				
	Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a>				
	Tissue Procurement: James Martin				
	cDNA Library preparation: Dr. M. Bento Soares, University of Iowa				
	cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa				
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa				
	Clone Distribution: Clone distribution information can be obtained				
	from Dr. M. Bento Soares, <a href="mailto:bento-soares@uiowa.edu">bento-soares@uiowa.edu</a>				
	Seq primer: M13 FORWARD				
	POLYA=Yes.				

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FEATURES
source
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FH1-bfu-m-08-0-UI"
/tissue_type="Cell Line"
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/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FH1"
/note="Organ: Chondrosarcoma; Vector: pT7T3-Pac (Pharmacia
) with a modified polylinker; Site 1: EcoR I; Site 2: Not
I; NCI CGAP_FH1 is a normalized cDNA library obtained from
a cell line derived from grade I chondrosarcoma tissue.
The library was constructed and normalized according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is AGAATCCGCG. The cell line

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was provided by Dr. James Martin from the University of Iowa.									
TAG_L1B=UI-H-FH1									
TAG_T1SUE=Human Chondrosarcoma Cell Line C88 - Grade 1 Chondrosarcoma									
TAG_SEQ=AGAAATCGGC"									
BASE COUNT	195 a	140 c	144 g	219 t	2 others				
ORIGIN									
Query Match	35.5%	Score 687.6;	DB 13;	Length 700;					
Best Local Similarity	99.0%;	Pred. No. 6.4e-100;							
Matches 690;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0;					
QY	857	AGCCGAGTCCACTGAGCAGCAAGGAGCTGAGTGAGCGCTTTTGACGAAAAGGCTAAGAA	916						
Db	700	AGCCGAGTCCACTGAGCAGCAAGNGACTGAGTGACCTTNTGACGAAAAGGCTAAGAA	64						
QY	917	AAAGGAAACCATTTCTAAACACACACAGAAACCTGTCCTCAATGCTTTGGGAACTGTGTTT	976						
Db	640	AAAGGAAACCATTTCTAAACACACAGAAACCTGTCCTCAATGCTTTGGGAACTGTGTTT	581						
QY	977	ATTGCTATAATGGGTGCTCCCAAAATGGGTAACTTAGACTTTCAGAGAGAAATGACGACAGAG	1036						
Db	580	ATTGCTATAATGGGTGCTCCCAAAATGGGTAACTTAGACTTTCAGAGAGAAATGACGACAGAG	521						
QY	1037	CAAAAGGAGAAATCTGGCTGTCTTCCATTTTCTCATCTCTGTTATCTCAGGTGAGCTGGTAGA	1096						
Db	520	CAAAAGGAGAAATCTGGCTGTCTTCCATTTTCTCATCTCTGTTATCTCAGGTGAGCTGGTAGA	461						
QY	1097	GGGGAGACATTAGAAAAAAATGAAACAAACAAACAAATCTAATAGGTGAGGTACGTGAGGCC	1156						
Db	460	GGGGAGACATTAGAAAAAAATGAAACAAACAAACAAATCTAATAGGTGAGGTACGTGAGGCC	401						
QY	1157	TGGGAGTCTCTTGACTCCACTACTTAATTCGGTTTATGAGAGAAACCTTTCAAATTTCTTTT	1216						
Db	400	TGGGAGTCTCTTGACTCCACTACTTAATTCGGTTTATGAGAGAAACCTTTCAAATTTCTTTT	341						
QY	1217	TATTAGNAGGGCCAGCTTACTGTTGGTGGGAAATTTGCCAAATATAGTTTAATAGAAAGTT	1276						
Db	340	TATTAGNAGGGCCAGCTTACTGTTGGTGGGAAATTTGCCAAATATAGTTTAATAGAAAGTT	281						
QY	1277	GGGCAATTTTCAACCCCATTTTCTGTGGGTCCACATTTGCAATTTGCAATTTGCAATTTGCAATTT	1336						
Db	280	GGGCAATTTTCAACCCCATTTTCTGTGGGTCCACATTTGCAATTTGCAATTTGCAATTTGCAATTT	221						
QY	1337	GCTGCTGACACCGAGTACTAGCCAGCAGCAAAAGCGAGGTAGCCCTGGAATTCGTTT	1396						
Db	220	GCTGCTGACACCGAGTACTAGCCAGCAGCAAAAGCGAGGTAGCCCTGGAATTCGTTT	161						
QY	1397	CTGCTCTTTACATTTCTTTTAAATTAAGCMTTATGTCGTCAGTCCCTACTGAGTACTCTTT	1456						
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QY	1457	TCCTCTCCCTCTCTGAAATTTAAATTCCTTCAACTTGCATTTTGCAGGATTAACACATTTTC	1516						
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QY	1517	ACTGTGATGTATATGTGTTGCAGNAGAAAGAAAAA	1553						
Db	40	ACTGTGATGTATATGTGTTGCAGNAGAAAGAAAAA	4						

RESULT 5	BM983868/c	BM983868	674 bp	mRNA	linear	EST 20-FEB-2003
LOCUS		UI-CF-DUI-aaw-b-04-0-UI.s1	UI-CF-DUI	Homo sapiens	cdna clone	
DEFINITION		UI-CF-DUI-aaw-b-04-0-UI 3', mRNA sequence.				
ACCESSION		BM983868				
VERSION		BM983868.1	GI:19608810			
KEYWORDS		EST.				
SOURCE		Homo sapiens (human)				
ORGANISM		Homo sapiens				
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				





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/clone_lib="NCI CGAP DHL"
/notes="Organ: Lung; Vector: pTT3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI_CGAP_DHL is a normalized cDNA library containing the
following tissue(s): VS-8 Cell line from Metastatic
Chondrosarcoma in Lung. The library was constructed
according to Bernaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dr primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pTT3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is AGATCATGTC.
TAG LIB=UI-H-DHL
TAG_TISSUE=lung
TAG_SEQ=AGATCATGTC"
BASE COUNT      220 a 106 c 139 g 194 t 2 others
ORIGIN
Query Match      31.9%; Score 617; DB 12; Length 661;
Best Local Similarity 98.2%; Pred. No. 1.2e-86;
Matches 644; Conservative 0; Mismatches 8; Indels 4; Gaps 2;
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DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
661 AAGTAAATAGAAAGTTGGCCAAATTCACCCCAATTTCTGTGTGGTTGGGCTCCCATTTGCA 603
QY 1321 ATGTTCAATGCCAGTGTCTGACACGACCGAGTACTAGCCAGCACAAAAGGAGGG 1380
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
602 ATGTTCAATGCCAGTGTCTGACACGACCGAGTACTAGCCAGCACAAAAGGAGGG 543
QY 1381 TAGCCTGAATTCCTTCTGCTCTTTACATTTCTTTTAAATAGCATTTAGTCTCAGTC 1440
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QY 1441 CCTACTGAGTACTCTTCTCTCCCTCTCTGAAATTAATTTCTTCAACTTGAATTTGC 1500
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
482 CCTACTGAGTACTCTTCTCTCCCTCTCTGAAATTAATTTCTTCAACTTGAATTTGC 423
QY 1501 AAGGATTACATTTCACTGTGATATATTTGTTGCGAGNAGAAAGAAAGTGTCTT 1560
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
422 AAGGATTACATTTCACTGTGATATATTTGTTGCGAGNAGAAAGTGTCTT 366
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365 TGTTTAAATTTACTTGGTTTGTGAATCCATCTTGTCTTTTCCCATTTGGAATAGTCAAT 306
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305 AACCCATCTCTGAAGTGTGAGAAACATCTGAAGAGTGTATCTATCAGCATCTGACAGG 246
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185 AATTAGTTGGGTTCTCTACATGCATAACAAACCCCTGCTCCAAATCTGTCCATAAAGTC 126
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DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
125 TGTGACTTGAAGTTTGTAGTCAGCACCCCAACCACTTATTTTCTATGTTGTTTTTGA 66
QY 1861 ACATATGAGTTTTCGAAATTAAGTACCCATGCTTTTATTAATAAATAAATAA 1916
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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DEFINITION RCI-OT0083-220300-021-f10 OT0083 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AW886523
VERSION    AW886523.1 GI:8048535
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 678)
AUTHORS   Dias Neto E., Garcia Correa R., Verjovski-Almeida S., Briones M.R.,
            Nagai M.A., da Silva W. Jr., Zago M.A., Bordin S., Costa F.F.,
            Goldman G.H., Carvalho A.F., Matsukuma A., Bala G.S., Simpson D.H.,
            Brunstein A., deoliveira P.S., Bucher P., Jongeneel C.V., O'Hare
            M.J., Soares F., Brentani R.R., Reis L.F., de Souza S.J. and
            Simpson A.J.
TITLE      Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE    20202663
PUBMED     10737800
COMMENT    Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=RC1-OT0083-220
            300-021-f10&t3=2000-03-22&t4=1)
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                /clone_lib="OT0083"
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                from ORESTES PCR (U.S. Letters Patent application No. 196
                716 - Ludwig Institute for Cancer Research) profiles
                into the puc 18 vector. Reverse transcription of tissue
                mRNA and cDNA amplification were performed under low
                stringency conditions."
BASE COUNT      196 a 145 c 163 g 174 t
ORIGIN
Query Match      31.0%; Score 600; DB 10; Length 678;
Best Local Similarity 97.4%; Pred. No. 5.9e-86;
Matches 631; Conservative 0; Mismatches 15; Indels 2; Gaps 2;
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2 GGCAGAGCTTACTGA-GCTGTCCAGTGGAGGCTCATGGTGGACATGGAAGAAGGC 60
QY 841 AGCTAGGCCCTGGGAGGCCAGTCCACTGAGCAAGGAGCTGAGTGAGCCTTTTGC 900
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
61 AGCTAGGCCCTGGGAGGCCAGTCCACTGAGCAAGGAGCTGAGTGAGCCTTTTGC 120
QY 901 AGGAAAGGCTTAAGAAAAGGAAAACCATTTCTAAACACACAAAGAACTGTCCAAATGC 960
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121 AGGAAAGGCTTAAGAAAAGGAAAACCATTTCTAAACACACAAAGAACTGTCCAAATGC 180
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181 TTTGGGAACCTGTGTTTATTGCTTATATGGTGTCCCAAAATGGGTAACTTAGACTTCAGA 240
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Db 241 GAGAAATGACAGAGACAAAGGAGAAATCTGGCTGCTTCCATTTTCAATTTCTGTTATCT 300  
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QY 1321 AATGTTCAATGCCAGCTGCTGCTGACACCGACCGAGTACTAGCCAGCACAAAGGCGAGG 1380  
Db 541 AATGTTCAATGCCAGCTGCTGCTGACACCGACCGAGTACTAGCCAGCACAAAGGCGAGG 600  
QY 1381 TAGCCTGAATGCTTTCTGCTCTTTTACATTTCTTTTAAATAGCAAT 1428  
Db 601 TAGCCTGAATGCTTTCTGCTCTTTTCAATTTCTTTTAAATAGCAAT 647

RESULT 8  
BU619261/c  
LOCUS  
DEFINITION  
UI-H-FH1-bfr-b-10-0-UI.s1 NCI CGAP FH1 Homo sapiens cDNA clone  
UI-H-FH1-bfr-b-10-0-UI 3', mRNA sequence.  
ACCESSION  
BU619261  
VERSION  
BU619261.1 GI:23285476  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 608)  
REFERENCE  
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
AUTHORS  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL  
Unpublished  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)  
Tissue Procurement: James Martin  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained  
from Dr. M. Bento Soares, [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
source  
1..608  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FH1-bfr-b-10-0-UI"  
/issue\_type="Cell Line"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI CGAP\_FH1"  
/notes="Organ: Chondrosarcoma; Vector: pT73-Pac (Pharmacia)  
I; with a modified polylinker; Site 1: EcoR I; Site 2: Not  
I; NCI CGAP FH1 is a normalized cDNA library obtained from  
a cell line derived from grade I chondrosarcoma tissue.  
The library was constructed and normalized according to  
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,  
1996. First strand cDNA synthesis was primed with an  
oligo-dT primer containing a Not I site. Double stranded

cDNA was ligated to an EcoR I adaptor, digested with Not  
I, and cloned directionally into pT73-Pac vector. The  
oligonucleotide used to prime the synthesis of  
first-strand cDNA contains a library tag sequence that is  
located between the Not I site and the (dT)18 tail. The  
sequence tag for this library is AGAATCCGCG. The cell line  
was provided by Dr. James Martin from the University of  
Iowa.  
TAG LIB=UI-H-FH1  
TAG TISSUE=Human Chondrosarcoma Cell Line CS8 - Grade 1  
Chondrosarcoma  
TAG\_SEQ=AGAATCCGCG  
BASE COUNT 184 a 121 c 124 g 179 t  
ORIGIN  
Query Match 31.0%; Score 599.2; DB 13; Length 608;  
Best Local Similarity 99.3%; Pred. No. 8.3e-86;  
Matches 601; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 949 CTGTCCAAATGCTTTGGGAACTGTGTTTATTCCTATATATGGGTCCCCAAAATGGGTAAAC 1008  
Db 608 CTGTCCAAATGCTTTGGGAACTGTGTTTATTCCTATATATGGGTCCCCAAAATGGGTAAAC 549  
QY 1009 CTAGACTTCAGAGAAATGAGCAGAGAGCAAAAGGAGAAATCTGGCTGTCTTCCATTTTC 1068  
Db 548 CTAGACTTCAGAGAAATGAGCAGAGAGCAAAAGGAGAAATCTGGCTGTCTTCCATTTTC 489  
QY 1069 ATTCTGTTATCTCAGGTGAGCTGGTAGAGGGGAGACATTAGAAAAAATGAAACAAACAA 1128  
Db 488 ATTCTGTTATCTCAGGTGAGCTGGTAGAGGGGAGACATTAGAAAAAATGAAACAAACAA 429  
QY 1129 ACAATTAATAGAGTACGCTGAGCGCTGGGAGTCTCTTGACTCCACTACTTAATTCGG 1188  
Db 428 ACAATTAATAGAGTACGCTGAGCGCTGGGAGTCTCTTGACTCCACTACTTAATTCGG 369  
QY 1189 TTTAGTGAGAAACCTTTTCAATTTCTTTTATTAGAGGGCCAGCTTACTGTTGGTGCAA 1248  
Db 368 TTTAGTGAGAAACCTTTTCAATTTCTTTTATTAGAGGGCCAGCTTACTGTTGGTGCAA 309  
QY 1249 AATTCGCCAACATAAGTAAATAGAAAGTTGGCAATTTTCAACCCCATTTTCTGTTGGTGG 1308  
Db 308 AATTCGCCAACATAAGTAAATAGAAAGTTGGCAATTTTCAACCCCATTTTCTGTTGGTGG 249  
QY 1309 CTCCACATTTGCAATGTTTCAATGCCAGCTGCTGCTGACACCGGAGTACTAGCCAGCA 1368  
Db 248 CTCCACATTTGCAATGTTTCAATGCCAGCTGCTGCTGACACCGGAGTACTAGCCAGCA 189  
QY 1369 CAAAAGGCGAGGTAGCTGAATGCTTTCTGCTCTTTTACATTTCTTTTAAATAAGCAAT 1428  
Db 188 CAAAAGGCGAGGTAGCTGAATGCTTTCTGCTCTTTTACATTTCTTTTAAATAAGCAAT 129  
QY 1429 TAGTGCTCAGTCCCTACTGAGTACTCTTCTCTCCCTCTCTGAAATTAATTTCTTCAA 1488  
Db 128 TAGTGCTCAGTCCCTACTGAGTACTCTTCTCTCCCTCTCTGAAATTAATTTCTTCAA 69  
QY 1489 CTTCGCAATTTGCAAGGATTACACATTTCACTGTGATATATTGTTGTCAGNGAAAAA 1548  
Db 68 CTTCGCAATTTGCAAGGATTACACATTTCACTGTGATATATTGTTGTCAGNGAAAAA 9  
QY 1549 AAAAA 1553  
Db 8 AAAAA 4  
RESULT 9  
CA430903/c  
LOCUS  
DEFINITION  
UI-H-FH1-bge-i-17-0-UI.s1 NCI CGAP FH1 Homo sapiens cDNA clone  
UI-H-FH1-bge-i-17-0-UI 3', mRNA sequence.  
ACCESSION  
CA430903  
VERSION  
CA430903.1 GI:24793629  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)



[illegible]

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
The following repetitive elements were found in this cDNA  
sequence: 1-30, >AT rich#Low\_complexity (matched complement)  
Seq primer: M13 FORWARD  
POLYA=Yes.

	FEATURES	SOURCE
1	100% Pure Cotton	USA
2	Machine Washable	India
3	Soft Touch Fabric	Bangladesh
4	Available in Multiple Colors	Pakistan
5	Durable Construction	Vietnam
6	Eco-Friendly Dyes	Thailand
7	Comfortable Fit	Malaysia
8	Long-Lasting Quality	Philippines
9	Stylish Design	Indonesia
10	Easy Care Instructions	Sri Lanka

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1. .663
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:5823649"
/tissue_type="Metastatic"
/dev_stage="Adult"
/lab_host="DH10B (Life T
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/Clone\_1115="NCI\_CGAP\_DHI1"  
/notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP DHI1 is a normalized cDNA library containing the following tissue(s): VS-8 Cell line from Metastatic Chondrosarcoma in Lung. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the ATC18 tail. The sequence tag for this library is AGATCATTCG.

BASE COUNT	219 a	106 c	140 g	197 t	1 others
TAG_SEQ=AGATCATTTGC"					
TAG_1330E-11m9					

Query Match 30.0%; Score 581.4; DB 12; Length 663;  
Best Local Similarity 97.3%; Pred. No. 5.5e-83;  
Matches 623; Conservative 0; Mismatches 12; Indels 5; Gaps 3;

	Qy	1278	GCCAAATTCACCCCAATTTTCTGTGTTGGGCTCACATTGGAATGTTCAATGCCACGTG	1337
	Db	645	GCCAAATTTTCACCCATTCTGTGGT-TGGGCTCCACAATTGGAATGTTCAATGCCACGTG	587
	Qy	1338	CTGCTGCACACCGACCGAGTAGTACTGCCAGCACAAGA-GCAGGGTAGCCTGGAATTGCTTTT	1396
	Db	586	CTGCTGCACACCGACCGGAGTACTGCCAGCACAAGAAGNGCAGGTAGCCTGGAATTGCTTTT	527
	Qy	1397	CTGCTCTTTTCAATTTCTTTTTAAAAATAAGCATTTAGTGTCTCAGTCCCTACTGAGTACTCTT	1456
	Db	526	CTGCTCTTTTCAATTTCTTTTTAAAATAAGATTTAGTGTCTCAGTCCCTACTGAGTACTCTT	467
	Qy	1457	TCTCTCCCCCTCTGAAATTTAATTTCTTTCAACTTTGCAATTTGCAAGGATTACACATTTTC	1516
	Db	466	TCTCTCCCCCTCTGAAATTTAATTTCTTTTCAACTTTGCAATTTGCAAGGATTACACATTTTC	407
	Qy	1517	ACTGTGATGTATATTGTGTTGCAGNAAAAAGAAAAAGTGTCTTTGTTTAAAAATTACTTTG	1576
	Db	406	ACTGTGATGTATATTGTGTGCA---AAAAAAAAAAAGTGTCTTTGTTTAAAAATTACTTTG	350
	Qy	1577	GTTTGTGTAATCCATCTTCTTTTTTCCCACTTGGAACTAGTCATTAAACCCTCTCTGNACT	1636
	Db	349	GTTTGTGTAATCCATCTGCTTTTTTCCCATTTGGAATCTAGTCATTAAACCCTCTCTGNACT	290
	Qy	1637	GGTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTGCACAGGTGAATTTGGATGGTTCT	1696
	Db	289	GGTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTGCACAGGTGAATTTGGATGGTTCT	230
	Qy	1697	CAGAACCAATTTCACCACAGACGCTGTTTCTATCTCTGTTTAAATAAATAGTTTGGGTTCT	1756

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Db      229  CAGAACCAATTTCAACCCAGACAGCCGTTTCTATCTGTTTAAATAAATTAGTTGGTTCT 170
QY      1757  CTACATGATACAAACCTGCTCAATCTGTCATATAAAAGTCTGTGACTTCAAGTTTAA 1816
Db      169  CTACATGATACAAACCTGCTCAATCTGTCATATAAAAGTCTGTGACTTCAAGTTTAA 110
QY      1817  CTCAGCACCCCAACCAACTTATTTTCTATGTTTGTGTTTGTGACATATGAGTGTGTTG 1876
Db      109  CTCAGCACCCCAACCAACTTATTTTCTATGTTTGTGTTTGTGACATATGAGTGTGTTG 50
QY      1877  AAAATAAGTACCCATGCTTTTATTAATAAANAATAAAAAA 1916
Db      49  AAAATAAGTACCCATGCTTTTATTAAGATTAATAAAAAA 10

RESULT 12
LOCUS   BE973555
DEFINITION 601680918f1 NIH MGC_83 Homo sapiens cDNA clone IMAGE:3950932 5', mRNA sequence.
ACCESSION BE973555
VERSION BE973555
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1. (bases 1 to 681)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lln.gov
Plate: LLC818 row: d column: 05
High quality sequence stop: 614.
FEATURES
Location/Qualifiers
1..681
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3950932"
/lab_host="NIH MGC 83"
/clone_lib="NIH MGC 83"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggcc
); 5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ATTCAGAGCGGCGGACATG-dt(30)BN-3'
(sequence: 5'-ATTCAGAGCGGCGGACATG-dt(30)BN-3'
where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
BASE COUNT 198 a 144 c 147 g 192 t
ORIGIN

Query Match 28.6%; Score 554.2; DB 10; Length 681;
Best Local Similarity 96.5%; Pred. No. 1.2e-78;
Matches 599; Conservative 0; Mismatches 18; Indels 4; Gaps 3;

QY 849 CCCTGGGGAGCCAGTCCAGTCCAGGACGAGGAGTGGAGCTTTTCAGGAAAAAG 908
Db 1 CCCTGGGGAGCCAGTCCAGTCCAGGACGAGGAGTGGAGCTTTTCAGGAAAAAG 60
QY 909 GCTAAGAAAAAGAAACCAATTTCTAAACACAAAGAACTGTCCAAATGCTTTGGAA 968

```

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Db      61  GCTAAGAAAAAGAAACCAATTTCTAAACACAAAGAAATGTCTTCAAAATGCTTTGGAA 120
QY      969  CTGTGTTTATTTGCTTAATATGCGTCCCAAAATGGGTAACTAGACTTCCAGAGAGATGA 1028
Db      121  CTGTGTTTATTTGCTTAATATGCGTCCCAAAATGGGTAACTAGACTTCCAGAGAGATGA 180
QY      1029  GCAGAGAGCAAGAGAAATCTGGTGTCTCTTCCATTTTTCATTTCTGTATCTCAGGTGAG 1088
Db      181  GCAGAGAGCAAGAGAAATCTGGTGTCTCTTCCATTTTTCATTTCTGTATCTCAGGTGAG 240
QY      1089  CTGCTAGAGGGGAGACATTAGAAAAAATGAAAAACACAAACAATTAATAGAGTACG 1148
Db      241  CTGCTAGAGGGGAGACATTAGAAAAAATGAAAAACACAAACAATTAATAGAGTACG 300
QY      1149  CTGAGGCTTGGAGTCTTGTGCTCACTCACTTAATTCCTGTTAGTGAGAAACCTTTCAA 1208
Db      301  CTGAGGCTTGGAGTCTTGTGCTCACTCACTTAATTCCTGTTAGTGAGAAACCTTTCAA 360
QY      1209  TTTTCTTTTATTAGAGGGCCAGCTTACTGTGTGGTGGCAAAATTCGCCAACAATAAGTTAA 1268
Db      361  TTTTCTTTTATTAGAGGGCCAGCTTACTGTGTGGTGGCAAAATTCGCCAACAATAAGTTAA 420
QY      1269  AGAAAGTTGGCAATTTCACTCACTCACTTAATTCCTGTTAGTGAGAAACCTTTCAA 1328
Db      421  AGAAAGTTGGCAATTTCACTCACTCACTTAATTCCTGTTAGTGAGAAACCTTTCAA 480
QY      1329  TGCCACGTGCTGTGACACCGGAGTACTAGCCAGCAAAAGCAGGGTAGGCTGA 1388
Db      481  TGCCACGTGCTGTGACACCGGAGTACTAGCCAGCAAAAGCAGGGTAGGCTGA 539
QY      1389  ATTGCTTTCTGCTCTTTACATTTCTTTAAATAAGCAATTTAGTGTCTCAGTCCCTACTGA 1448
Db      540  ATGG--TTTCTGTCTTTACATTTCTTTAAATAAGCAATTTAGTGTCTCAGT--CTTACTGA 596
QY      1449  GTACTCTTTCTCTCCCTCTCT 1469
Db      597  GTACTCTTTCTCTCCCTCTCT 617

RESULT 13
LOCUS   AI989273
DEFINITION 2 prostate cancer cell line LNCap Homo sapiens EST 02-SEP-2001
ACCESSION AI989273
VERSION AI989273.1 GI:15421021
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Zhang, J.S. and Smith, D.I.
High throughput screening for androgen regulated genes in LNCap
cells: Identification of hAG-2 as an androgen regulated gene over
expressed in prostate adenocarcinoma
Unpublished
Contact: Zhang, Jin-San
Dept. Pathology and Lab Medicine
Mayo Clinic Cancer Center
200 1st St. SW, Rochester MN 55905, USA
Tel: 507-2660311
Fax: 507-2665193
Email: zhang.jinsan@mayo.edu.
Location/Qualifiers
1..563
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="prostate cancer cell line LNCap"
/note="prostate cancer metastasized to lymph node;
subtracted cDNA libraries from prostate cancer cell line
LNCap treated with androgen."
FEATURES
Source

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BASE COUNT	187 a	104 c	143 g	129 t	
ORIGIN					
Query Match	28.4%;	Score 550;	DB 9;	Length 563;	
Best Local Similarity	99.8%;	Pred. No.. 6e-78;			
Matches 561, Conservative	0;	Mismatches	0;	Indels	1; Gaps 1;
Qy	586	TTAAAAATACATAGCATTTAAATCCAAATCCATATTTAAAGACCTGACAGCTTGAGAAAGGT	645		
Db	3	TTAAAAATACATAGCATTTAAATCCAAATCCATATTTAAAGACCTGACAGCTTGAGAAAGGT	62		
Qy	646	CACCTACTGCATTTATAGACCTCTGGTGGTTCCTGCTGTACGTTTGAAGTCTGACACATC	705		
Db	63	CACCTACTGCATTTATAGACCTCTGGTGGTTCCTGCTGTACGTTTGAAGTCTGACACATC	122		
Qy	706	CTTGAGAAATCTTTGCATGCGAGGAGGTAAAGAGGTATTTGGATTTTTCACAGAGGAAGAACA	765		
Db	123	CTTGAGAAATCTTTGCATGCGAGGAGGTAAAGAGGTATTTGGATTTTTCACAGAGGAAGAACA	182		
Qy	766	CAGCGCAGAAATGAAGGGCCAGGCTTACTGAGGCTGTCCAGTGGAGGGCTCATGGGTGGGA	825		
Db	183	CAGCGCAGAAATGAAGGGCCAGGCTTACTGGA - GCTGTCCAGTGGAGGGCTCATGGGTGGGA	241		
Qy	826	CATGGAAAAGAGGACGACCTAGGCCCTGGGGAGGCCAGTCCACTGACGACGACGAGGACT	885		
Db	242	CATGGAAAAGAGGACGACCTAGGCCCTGGGGAGGCCAGTCCACTGACGACGACGAGGACT	301		
Qy	886	GAGTGAAGCCTTTTTCAGAGAAAAGGCTTAAGAAAAAGGAAAAACCATTTCTAAAAACACAAACAAG	945		
Db	302	GAGTGAAGCCTTTTTCAGAGAAAAGGCTTAAGAAAAAGGAAAACCATTTCTAAAAACACAAACAAG	361		
Qy	946	AAACTGTGCTCAAAATGCTTTGGGAACTGTGTTTATTTAGTCCCTATAATGGGTCCCCAAATCGGT	1005		
Db	362	AAACTGTGCTCAAAATGCTTTGGGAACTGTGTTTATTTAGTCCCTATAATGGGTCCCCAAATCGGT	421		
Qy	1006	AACTAGACATTCAGAGAGATGACGACAGAGCAGCAAGGAGAAATCTGGCTGTCTTCCATT	1065		
Db	422	AACCTAGACTTCAGAGAGATGACGACAGAGCAGCAAGGAGAAATCTGGCTGTCTTCCATT	481		
Qy	1066	TTCAATTCGTGTATCTCAGGTGAGCTGGTGTAGAGGGGAGACATTTAGAAAAAAATGAAAAACAC	1125		
Db	482	TTCAATTCGTGTATCTCAGGTGAGCTGGTGTAGAGGGGAGACATTTAGAAAAAAATGAAAAACAC	541		
Qy	1126	AAAAACAATTTACTAATGAGGTAC	1147		
Db	542	AAAAACAATTTACTAATGAGGTAC	563		

RESULT 14  
 BF679599  
 LOCUS  
 DEFINITION  
 BF679599 565 bp mRNA linear EST 21-DEC-2000  
 602154041F1 NIH\_MGC\_83 Homo sapiens cDNA clone IMAGE:4294931 5',  
 mRNA sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NTH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-x@mail.nih.gov](mailto:cgapbs-x@mail.nih.gov)  
 Tissue Procurement: CLONTECH Laboratories, Inc.  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

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Plate: LLCml145 row: a column: 12
High quality sequence stop: 563.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4294931"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_83"
/notes="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site 1: Sfil (ggcgcctatggcc); Site 2: Sfil (ggccattatggcc
); 5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCCGAGCGCCGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.4 kb (range 0.5-4.0 kb), 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
178 a 111 c 144 g 132 t

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Query Match	27.5%;	Score 532;	DB 10;	Length 565;
Best Local Similarity	99.5%;	Pred. No. 4.4e-75;		
Matches 565;	Conservative 0;	Mismatches 0;	Indels 3;	Gaps 3;

  

Qy	751	CACAGAGGAAGAACACAGCGSCAGAACTGAAGGGCCAGGCTTACTAGAGCTGTGCAGTGGAG	810
Db	1	CACAGAGGAAGAACACAGCGCAGAACTGAAGGGCCAGGCTTACTGA- GCTGTCCAGTGGAG	59
Qy	811	GGCTCATGGGTGGGACATGAAAAAGAGGAGGAGCTTAGGCCCTCGGGAGGCCAGTCCAATG	870
Db	60	GGCTCATGGGTGGGACATGGAAGAAGAGGAGGAGCTTAGGCCCTCGGGAGGCCAGTCCAATG	119
Qy	871	AGCAAGCAAGGGAAGTGAAGTGGCTTTTCAGAGAAAGGCTAAGAAAGGAAAGCAAAACCAATT	930
Db	120	AGCAAGCAAGGGAAGTGAAGTGGCTTTTCAGAGAAAGGCTAAGAAAGGAAAGCAAAACCAATT	179
Qy	931	CTAAAAACAAACAGAAACCTGTCCAAATGCTTTGGGAACTGTGTTATTGCCCTATAATGG	990
Db	180	CTAAAAACAAACAGAAACCTGTCCAAATGCTTTGGGAACTGTGTTATTGCCCTATAATGG	239
Qy	991	GTCCCCAAAATGGGTAACTTAGACTTCACAGAGAAATGAGCAGAGAGCAAAAGGAGAAATCT	1050
Db	240	GTCCCCAAAATGGGTAACTTAGACTTCACAGAGAAATGAGCAGAGAGCAAAAGGAGAAATCT	299
Qy	1051	GGCTGTCTCTTCCATTTTTCATCTCTGTTATCTCAGGTGAGCTGGTAGAGGGGAGACATTAGA	1110
Db	300	GGCTGTCTCTTCCATTTTTCATCTGTTATCTCAGGTGAGCTGGTAGAGGGGAGACATTAGA	359
Qy	1111	AAAAAATGAACAAACAAAAACAATTTACTAATGAGGTACGCTGAGGCCCTGGGAGTCTCTTTGA	1170
Db	360	AAAAAATGAACAAACAAAAACAATTTACTAATGAGGTACGCTGAGGCCCTGGGAGTCTCTTTGA	419
Qy	1171	CTCCACTACTTAATTCGGTTTAGTGAAACCTTTTCAATTTCTTTTATTATAGAGGGGCCA	1230
Db	420	CTCCACTACTTAATTCGGTTTAGTGAAACCTTTTCAATTTCTTTTATTATAGAGGGGCCA	479
Qy	1231	GCCTTACTGTTGGTGCCAAAATTCGCCAACATAAGTTAATAGAAAAGTTGGCCAAATTTACACC	1290
Db	480	GCCTTACTG- TGGTGGCANAATTCGCCAACATAAGTTAATAGAAAAGTTGGCCAAATTTACACC	538
Qy	1291	CATTTTCTGTGGTTTGGGCTCCACATG	1318
Db	539	CATTTTCTGTGG- TTGGGCTCCACATG	565

RESULT 15					
AI620178/c					
LOCUS	AI620178	538 bp	mRNA	linear	EST 15-DEC-1999
DEFINITION	tu54a11.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2254844 3', mRNA sequence.				



ACCESSION AI620178 GI:4629304  
 VERSION RST.  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 538)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 found through the I.M.A.G.E. Consortium/LINL at:  
[www-bio.lini.gov/bbrp/image/image.html](http://www-bio.lini.gov/bbrp/image/image.html)  
 Insert Length: 825 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 456  
 POLYA=No.

## FEATURES

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 /notes="Organ: Prostate; Vector: pT7T3D-Pac (Pharmacia)  
 with a modified polylinker; Plasmid DNA from the  
 normalized library NCI CGAP Pr22 was prepared, and ss  
 circles were made in vitro. Following HAP purification,  
 this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (clones IDs  
 985608-986759, 1101192-1101959, and 1217928-1220615).  
 Subtraction by Bento Soares and M. Fatima Bonaldo."  
 BASE COUNT 190 a 84 c 113 g 151 t  
 ORIGIN

Query Match 27.0%; Score 521.8; DB 9; Length 538;  
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 QY 1484 TTCACTTGGCAATTTGCAAGGATTACACATTTCACTGTGATGATATTGTTGCA 1543  
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 QY 1604 CATTGCACTAGTCAATTAACCATCTCTGAAGTGTAGAAAAACATCTGAAGCTAGTC 1663  
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 QY 1904 A 1904  
 Db 1 A 1

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